

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 13, 2003, 21:41:37 ; Search time 1093 Seconds  
(without alignments)  
3488.076 Million cell updates/sec

Title: US-09-661-658B-2

Perfect score: 131  
Sequence: 1 gctctagatataagtgactt.....atgcctaacgactatccctt 131

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_da:\*

2: gb\_hlg:\*

3: gb\_in:\*

4: gb\_cm:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_pl:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vl:\*

15: em\_da:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_of:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vl:\*

30: em\_hlg\_hum:\*

31: em\_hlg\_inv:\*

32: em\_hlg\_other:\*

33: em\_hlg\_mus:\*

34: em\_hlg\_pln:\*

35: em\_hlg\_rtd:\*

36: em\_hlg\_mam:\*

37: em\_hlg\_vtl:\*

38: em\_sy:\*

39: em\_hlg\_hum:\*

40: em\_hlg\_mus:\*

41: em\_hlg\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	131	100.0	131	6	AX379337
2	127.4	97.3	131	6	AX379340
3	127.4	97.3	131	6	AX427105
4	123	93.9	128	6	AX427121
5	119	90.8	130	6	AX427102
6	109	83.2	133	6	AX427122
7	107	81.7	129	6	AX427124
8	87	66.4	119	6	AX427123
9	86.4	66.0	117	6	AX427126
10	83.4	63.7	115	6	AX427125
11	82.2	62.7	122	6	AX427131
12	81.4	62.1	107	6	AX427129
13	80.6	61.5	122	6	AX427116
14	79.8	60.9	107	6	AX427130
15	78.4	59.8	510	7	AP133973
16	78.4	59.8	2162	7	PF14FRDPI
17	78.4	59.8	168903	7	AF158101
18	78.2	59.7	124	6	AX427132
19	69.2	52.8	97	6	AX427120
20	49.6	37.9	144	6	AX427127
21	45.8	35.0	140	6	AX427128
22	37.2	28.4	59	6	AR209847
23	37.2	28.4	123	6	AR209841
24	37.2	28.4	123	6	AR209845
25	37.2	28.4	123	6	AR209847
26	37.2	28.4	125	6	AR209844
27	37.2	28.4	141	6	AR209845
28	37.2	28.4	149	6	AR209845
29	37.2	28.4	282	6	AR209845
30	34.6	26.4	137150	2	AC125856
31	34.4	26.3	216032	2	AC095703
32	34.4	25.6	95089	2	AC010406
33	33.6	25.6	183795	9	AC010423
34	33.6	25.6	282	6	AX034873
35	33	25.0	109273	2	AC130165
36	32.8	24.9	244	6	AX034878
37	32.6	24.9	283	6	AX034869
38	32.6	24.9	607	6	AX034876
39	32.2	24.6	40	6	AX034867
40	31.8	24.3	42	6	AX034890
41	31.8	24.3	45	6	AX034882
42	31.8	24.3	256	5	AX034875
43	31.8	24.3	608	5	AX034875
44	31.8	24.3	189693	2	AC119104
45	31.8	24.3	189693	2	AC119104

## ALIGNMENTS

RESULT 1  
AX379337  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

AX379337  
Sequence 2 from Patent WO0196541.  
AX379337.1 GI:19575177  
synthetic construct.  
synthetic construct.  
artificial sequences.

131 bp  
DNA  
linear  
PAT 18-MAR-2002

Ellington,A.D., Hesselberth,J., Marshall,K., Robertson,M.,  
Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.  
Allosterically regulated ribozymes  
Patent: WO 0196541-A 2 20-DEC-2001;

# BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)

FEATURES  
source  
1. 131  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Engineered Aptazyme"  
BASE COUNT 37 a 32 c 24 g 38 t  
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Query Match  
Best Local Similarity 100.0%; Score 131; DB 6; Length 131;  
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGAGTATTAAGTACTTATCTATCTAAGGGGAACTCTCTAGTAGA 60  
DB 1 GCCTGAGTATTAAGTACTTATCTATCTAAGGGGAACTCTCTAGTAGA 60  
QY 61 CAATCCCGTGTAAATTAATACAGCATGCTTGATGCCCTTGCGAGATAAATGCTTAAC 120  
DB 61 CAATCCCGTGTAAATTAATACAGCATGCTTGATGCCCTTGCGAGATAAATGCTTAAC 120  
QY 121 GACTATCCCTT 131  
DB 121 GACTATCCCTT 131

## RESULT 2

AX379340 131 bp DNA linear PAT 18-MAR-2002  
LOCUS AX379340  
DEFINITION Sequence 5 from Patent WO0196541.  
ACCESSION AX379340  
VERSION AX379340.1 GI:19575180  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct.  
artificial sequences.

REFERENCE  
AUTHORS  
1 Ellington,A.D., Hesselberth,J., Marshall,K., Robertson,M.,  
Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.  
Allosterically regulated ribozymes.  
Patent: WO 0196541-A 5 20-DEC-2001.  
JOURNAL  
BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)  
FEATURES  
Location/Qualifiers  
1. 131  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Engineered Aptazyme"

BASE COUNT 37 a 32 c 24 g 36 t 2 others  
ORIGIN

Query Match  
Best Local Similarity 97.3%; Score 127.4; DB 6; Length 131;  
Matches 128; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCTGAGTATTAAGTACTTATCTATCTAAGGGGAACTCTCTAGTAGA 60  
DB 1 GCCTGAGTATTAAGTACTTATCTATCTAAGGGGAACTCTCTAGTAGA 60  
QY 61 CAATCCCGTGTAAATTAATACAGCATGCTTGATGCCCTTGCGAGATAAATGCTTAAC 120  
DB 61 CAATCCCGTGTAAATTAATACAGCATGCTTGATGCCCTTGCGAGATAAATGCTTAAC 120  
QY 121 GACTATCCCTT 131  
DB 121 GACTATCCCTT 131

RESULT 3  
AX427105 131 bp DNA linear PAT 18-JUN-2002  
LOCUS AX427105  
DEFINITION Sequence 5 from Patent WO0196559.  
ACCESSION AX427105  
VERSION AX427105.1 GI:21530488

KEYWORDS  
SOURCE  
1. 131  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Oligonucleotides"

REFERENCE  
AUTHORS  
1 Ellington,A.D., Hesselberth,J., Marshall,K., Robertson,M.,  
Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.  
Regulatable, catalytically active nucleic acids  
Patent: WO 0196559-A 5 20-DEC-2001.  
JOURNAL  
Board of Regents, The University of Texas System (US)  
FEATURES  
Location/Qualifiers  
1. 131  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Oligonucleotides"

BASE COUNT 37 a 32 c 24 g 36 t 2 others  
ORIGIN

Query Match  
Best Local Similarity 97.3%; Score 127.4; DB 6; Length 131;  
Matches 128; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCTGAGTATTAAGTACTTATCTATCTAAGGGGAACTCTCTAGTAGA 60  
DB 1 GCCTGAGTATTAAGTACTTATCTATCTAAGGGGAACTCTCTAGTAGA 60  
QY 61 CAATCCCGTGTAAATTAATACAGCATGCTTGATGCCCTTGCGAGATAAATGCTTAAC 120  
DB 61 CAATCCCGTGTAAATTAATACAGCATGCTTGATGCCCTTGCGAGATAAATGCTTAAC 120  
QY 121 GACTATCCCTT 131  
DB 121 GACTATCCCTT 131

## RESULT 4

AX427121 128 bp DNA linear PAT 18-JUN-2002  
LOCUS AX427121  
DEFINITION Sequence 21 from Patent WO0196559.  
ACCESSION AX427121  
VERSION AX427121.1 GI:21530504  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct.  
artificial sequences.

REFERENCE  
AUTHORS  
1 Ellington,A.D., Hesselberth,J., Marshall,K., Robertson,M.,  
Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.  
Regulatable, catalytically active nucleic acids  
Patent: WO 0196559-A 21 20-DEC-2001.  
JOURNAL  
Board of Regents, The University of Texas System (US)  
FEATURES  
Location/Qualifiers  
1. 128  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide"

BASE COUNT 36 a 32 c 23 g 37 t  
ORIGIN

Query Match  
Best Local Similarity 100.0%; Score 123; DB 6; Length 128;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ATAAGTGACTTATTAATCTATCTAAGGGGAACTCTCTAGTAGACATCCG 68  
DB 6 ATAAGTGACTTATTAATCTATCTAAGGGGAACTCTCTAGTAGACATCCG 65  
QY 69 TGTAAATTAATACAGCATGCTTGATGCCCTTGCGAGATAAATGCTTAAC 128  
DB 69 TGTAAATTAATACAGCATGCTTGATGCCCTTGCGAGATAAATGCTTAAC 125  
QY 129 CTT 131





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REFERENCE
AUTHORS      1
              Ellington,A.D., Hesselberth,J., Marshall,K., Robertson,M.,
              Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.
TITLE
JOURNAL      Regulatable, catalytically active nucleic acids
              Patent: WO 0196559-A 29 20-DEC-2001;
              Board of Regents, The University of Texas System (US)
FEATURES
source
              1. 107
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="Oligonucleotide"
BASE COUNT   31 a      28 c      19 g      29 t
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Best Local Similarity 97.2%; Pred. No. 6,6e-17;
Matches 104; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 27 GTAATCTATCTAAAGGGGACCTCTAGTAGACAAATCCGCTAAATT-ATACCAGC 85
    |||||||
Db 1 GTAATCTATCTAAAGGGGACCTCTCTAGTAGACAAATCCGCTAAATTATACACAGC 60
    |||||||

QY 86 ATCGCTTGATGCCCTTGGCAG-ATAAATGCCCTAACGACTATCCCTT 131
    |||||||
Db 61 ATCGCTTGATGCCCTTGGCAGATAAATGCCCTAACGACTATCCCTT 107
    |||||||

RESULT 13
AX427116      122 bp      DNA      linear      PAT 18-JUN-2002
LOCUS
DEFINITION   Sequence 16 from Patent WO0196559.
ACCESSION    AX427116
VERSION      AX427116.1 GI:21530499
KEYWORDS
SOURCE       synthetic construct.
ORGANISM     synthetic construct
              artificial sequences.
REFERENCE
AUTHORS      1
              Ellington,A.D., Hesselberth,J., Marshall,K., Robertson,M.,
              Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.
TITLE
JOURNAL      Regulatable, catalytically active nucleic acids
              Patent: WO 0196559-A 16 20-DEC-2001;
              Board of Regents, The University of Texas System (US)
FEATURES
source
              1. 122
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="Oligonucleotide"
BASE COUNT   34 a      29 c      24 g      35 t
ORIGIN
Query Match  61.5%; Score 80.6; DB 6; Length 122;
Best Local Similarity 82.4%; Pred. No. 1.2e-16;
Matches 108; Conservative 0; Mismatches 14; Indels 9; Gaps 1;

QY 1 GCCGTAGTATAGGTGACTATATCTATCTATCTATCTAAAGGGGAACTCTTAGTAGA 60
    |||||||
Db 1 GCCGTAGTATAGGTGACTATATCTATCTATCTATCTAAAGGGGAACTCTTAGTAGA 60
    |||||||

QY 61 CAATCCCGTCTAAATTATACAGACATCGTCTTGATGCCCTTGGCAGATTAATGCTTAC 120
    |||||||
Db 61 CAATCCCGTCTAAATTATAGAGACTGCC-----CGGTTCTACATTAATGCTTAC 111
    |||||||

QY 121 GACTATCCCTT 131
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Db 112 GACTATCCCTT 122
    |||||||

RESULT 14
AX427130      107 bp      DNA      linear      PAT 18-JUN-2002
LOCUS
DEFINITION   Sequence 30 from Patent WO0196559.
ACCESSION    AX427130

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VERSION      AX427130.1 GI:21530513
KEYWORDS
SOURCE       synthetic construct.
ORGANISM     synthetic construct
              artificial sequences.
REFERENCE
AUTHORS      1
              Ellington,A.D., Hesselberth,J., Marshall,K., Robertson,M.,
              Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.
TITLE
JOURNAL      Regulatable, catalytically active nucleic acids
              Patent: WO 0196559-A 30 20-DEC-2001;
              Board of Regents, The University of Texas System (US)
FEATURES
source
              1. 107
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="Oligonucleotide"
BASE COUNT   29 a      28 c      19 g      31 t
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Query Match  60.9%; Score 79.8; DB 6; Length 107;
Best Local Similarity 96.3%; Pred. No. 2.3e-16;
Matches 103; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 27 GTAATCTATCTAAAGGGGAACTCTCTAGTAGACAAATCCGCTAAATT-ATACCAGC 85
    |||||||
Db 1 GTAATCTATCTAAAGGGGAACTCTCTAGTAGACAAATCCGCTAAATTGATACACAGC 60
    |||||||

QY 86 ATCGCTTGATGCCCTTGGCAG-ATAAATGCCCTAACGACTATCCCTT 131
    |||||||
Db 61 ATCGCTTGATGCCCTTGGTGTGCAATAAATGCCCTAACGACTATCCCTT 107
    |||||||

RESULT 15
AR013973      510 bp      DNA      linear      PAT 05-DEC-1998
LOCUS
DEFINITION   Sequence 1 from patent US 5773244.
ACCESSION    AR013973
VERSION      AR013973.1 GI:3971427
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unknown.
              Unclassified.
REFERENCE
AUTHORS      1 (bases 1 to 510)
              Ares,M. Jr. and Ford,E.E.
TITLE
JOURNAL      Methods of making circular RNA
              Patent: US 5773244-A 1 30-JUN-1998;
              Location/Qualifiers
FEATURES
source
              1. 510
              /organism="unknown"
BASE COUNT   153 a      80 c      109 g      168 t
ORIGIN
Query Match  59.8%; Score 78.4; DB 6; Length 510;
Best Local Similarity 98.8%; Pred. No. 7.7e-16;
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCGTAGTATAGGTGACTATATCTTGTAAATCTATCTAAAGGGGAACTCTTAGTAGA 60
    |||||||
Db 341 GCCGTAGTATAGGTGACTATATCTTGTAAATCTATCTAAAGGGGAACTCTTAGTAGA 400
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QY 61 CAATCCCGTCTAAATTATA 80
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Db 401 CAATCCCGTCTAAATTGTA 420
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Search completed: July 13, 2003, 22:53:39  
 Job time : 1094 secs





PT assays for detecting the presence of ligands or activation of an effector of RCANA.

XX Example 1; Page 40; 126pp; English.

CC The present invention relates to regulatable, catalytically active nucleic acids (RCANAs) which are regulated by polypeptides. These are useful for regulating gene expression, in assays for detecting the presence of ligands, for activation of an effector of RCANA, and in gene therapy. The present sequence is an oligonucleotide used in the construction of an RCANA.

SO Sequence 131 BP; 37 A; 32 C; 24 G; 38 T; 0 other;

Query Match 100.0%; Score 131; DB 24; Length 131;  
Best Local Similarity 100.0%; Pred. No. 5,4e-38;

Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGAGTAAAGGTGACTTAACTTAACTTAACTTAAAGGGGAACTCTTACTAGAC 60  
DB 1 GCCTGAGTAAAGGTGACTTAACTTAACTTAACTTAAAGGGGAACTCTTACTAGAC 60

QY 61 CAATCCGCTGCTAAATATATACAGCATCGCTTGATGCCCTTGCGAGATTAATGCCCTAAC 120  
DB 61 CAATCCGCTGCTAAATATATACAGCATCGCTTGATGCCCTTGCGAGATTAATGCCCTAAC 120

QY 121 GACTATCCCTT 131  
DB 121 GACTATCCCTT 131

RESULT 2

AAL43049 standard; DNA: 131 BP.

AC AAL43049;

DT 25-SEP-2002 (first entry)

DE Regulatable, catalytically active nucleic acid construction oligo #8.

KM Regulatable catalytically active nucleic acid; RCANA; ribozyme;

OS Synthetic.

PN WO200196559-A2.

PD 20-DEC-2001.

PF 14-JUN-2001; 2001WO-US19302.

PR 15-JUN-2000; 2000US-212097P.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L, Davidson E, Cox JC, Reidel T;

DR WPI: 2002-122216/16.

PT New regulatable, catalytically active nucleic acids (RCANA), useful in gene therapy (particularly for regulating gene expression), or in assays for detecting the presence of ligands or activation of an effector of RCANA.

XX Example 5; Page 68; 126pp; English.

CC The present invention relates to regulatable, catalytically active nucleic acids (RCANAs) which are regulated by polypeptides. These are useful for regulating gene expression, in assays for detecting the presence of ligands, for activation of an effector of RCANA, and in gene therapy. The present sequence is an oligonucleotide used in the

CC construction of an RCANA.

SO Sequence 131 BP; 37 A; 32 C; 24 G; 38 T; 0 other;

Query Match 100.0%; Score 131; DB 24; Length 131;  
Best Local Similarity 100.0%; Pred. No. 5,4e-38;

Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGAGTAAAGGTGACTTAACTTAACTTAACTTAAAGGGGAACTCTTACTAGAC 60  
DB 1 GCCTGAGTAAAGGTGACTTAACTTAACTTAACTTAAAGGGGAACTCTTACTAGAC 60

QY 61 CAATCCGCTGCTAAATATATACAGCATCGCTTGATGCCCTTGCGAGATTAATGCCCTAAC 120  
DB 61 CAATCCGCTGCTAAATATATACAGCATCGCTTGATGCCCTTGCGAGATTAATGCCCTAAC 120

QY 121 GACTATCCCTT 131  
DB 121 GACTATCCCTT 131

RESULT 3

ABN83045 standard; DNA: 131 BP.

AC ABN83045;

DT 16-AUG-2002 (first entry)

DE Aptazyme construct oligonucleotide gpTthP6.131.

KM Aptazyme; regulatable; aptamer; luciferase; cyclic AMP; gpTthP6.131; ss.

OS Unidentified.

PN WO200196541-A2.

PD 20-DEC-2001.

PF 15-JUN-2001; 2001WO-US19119.

PR 15-JUN-2000; 2000US-0661658.

PA (TEXA) UNIV TEXAS.

PI Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L, Davidson E, Cox JC, Reidel T;

DR WPI: 2002-090203/12.

PT Aptazyme construct for detecting the presence of ligands, comprises a regulatable group I intron aptamer oligonucleotide with a regulatory domain, and modulates their kinetic parameters in response to an effector.

XX Claim 7; Page 30; 42pp; English.

CC The sequence represents an oligonucleotide used in the invention in the construction of a group I regulatable aptazyme. The invention relates to a novel aptazyme construct comprising a regulatable group I intron aptamer oligonucleotide sequence having an allosterically regulatable target gene vary in response to the kinetic parameters of the aptazyme on a molecule with the regulatory domain, and the intron splicing reaction occurs in vitro. The aptazyme is useful: (1) in assays to detect the presence of ligands or to detect activation of an aptazyme by an effector; (2) in the identification, isolation and enhancement of allosteric effectors and of the allosterically regulatable aptazymes with which they interact; (3) to activate or repress a reporter gene (e.g. luciferase) containing an engineered intron in response to an endogenous activator; and (4) to monitor intracellular levels of proteins or small molecules such as cyclic AMP.



Sequence 131 BP; 37 A; 32 C; 24 G; 38 T; 0 other;

Query Match 100.0%; Score 131; DB 24; Length 131;

Best Local Similarity 100.0%; Pred. No. 5,4e-38; Mismatches 0; Indels 0; Gaps 0;

Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGAGTAAAGGACTTAACTTGTAACTATCTAAACGGGGAACCTCTAGTAGA 60  
 1 GCCTGAGTAAAGGACTTAACTTGTAACTATCTAAACGGGGAACCTCTAGTAGA 60  
 Db 1 GCCTGAGTAAAGGACTTAACTTGTAACTATCTAAACGGGGAACCTCTAGTAGA 60  
 QY 61 CAATCCCGTGAATTAATATACAGCATGCTTGAATGCCCTTGCGAGATAAATGCCCTAAC 120  
 61 CAATCCCGTGAATTAATATACAGCATGCTTGAATGCCCTTGCGAGATAAATGCCCTAAC 120  
 Db 61 CAATCCCGTGAATTAATATACAGCATGCTTGAATGCCCTTGCGAGATAAATGCCCTAAC 120  
 QY 121 GACTATCCCTT 131  
 121 GACTATCCCTT 131  
 Db 121 GACTATCCCTT 131

#### RESULT 4

ALA43033 standard; DNA: 131 BP.

ALA43033;

25-SEP-2002 (first entry)

Regulatable, catalytically active nucleic acid construction oligo #3.

Regulatable catalytically active nucleic acid; RCANA; ribozyme;

gene therapy; ds.

Synthetic.

Key Location/Qualifiers

FT misc\_feature 77 /tag= a

FT /note= "represents between 1 and 4 unknown nucleotides"

FT misc\_feature 108 /tag= b

FT /note= "represents between 1 and 4 unknown nucleotides"

MO200196559-A2.

14-JUN-2001; 2001MO-US19302.

15-JUN-2000; 2000US-212097P.

(TEXA ) UNIV TEXAS SYSTEM.

Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L;

Davidson E, Cox JC, Reidel T;

WPI: 2002-122216/16.

New regulatable, catalytically active nucleic acids (RCANA), useful in gene therapy (particularly for regulating gene expression), or in assays for detecting the presence of ligands or activation of an effector of RCANA

Example 2; Page 42; 126pp; English.

The present invention relates to regulatable, catalytically active nucleic acids (RCANAs) which are regulated by polypeptides. These are useful for regulating gene expression, in assays for detecting the presence of ligands, for activation of an effector of RCANA, and in gene therapy. The present sequence is an oligonucleotide used in the construction of an RCANA.

Sequence 131 BP; 37 A; 32 C; 24 G; 36 T; 2 other;

Query Match 97.3%; Score 127.4; DB 24; Length 131;

Best Local Similarity 97.7%; Pred. No. 1.1e-36; Mismatches 3; Indels 0; Gaps 0;

Matches 128; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCTGAGTAAAGGACTTAACTTGTAACTATCTAAACGGGGAACCTCTAGTAGA 60  
 1 GCCTGAGTAAAGGACTTAACTTGTAACTATCTAAACGGGGAACCTCTAGTAGA 60  
 Db 1 GCCTGAGTAAAGGACTTAACTTGTAACTATCTAAACGGGGAACCTCTAGTAGA 60  
 QY 61 CAATCCCGTGAATTAATATACAGCATGCTTGAATGCCCTTGCGAGATAAATGCCCTAAC 120  
 61 CAATCCCGTGAATTAATATACAGCATGCTTGAATGCCCTTGCGAGATAAATGCCCTAAC 120  
 Db 61 CAATCCCGTGAATTAATATACAGCATGCTTGAATGCCCTTGCGAGATAAATGCCCTAAC 120  
 QY 121 GACTATCCCTT 131  
 121 GACTATCCCTT 131  
 Db 121 GACTATCCCTT 131

#### RESULT 5

ABN83048 standard; DNA: 131 BP.

ABN83048;

16-AUG-2002 (first entry)

Aptazyme construct oligonucleotide Gp17H6pool.

Aptazyme; regulatable; aptamer; luciferase; cyclic AMP; Gp17H6pool; ss.

Unidentified.

Key Location/Qualifiers

FT misc\_feature 77 /tag= a

FT /note= "Base may be repeated 1-4 times"

FT misc\_feature 108 /tag= a

FT /note= "Base may be repeated 1-4 times"

MO200196541-A2.

20-DEC-2001.

15-JUN-2001; 2001MO-US19119.

15-JUN-2000; 2000US-0661658.

(TEXA ) UNIV TEXAS.

Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L;

Davidson E, Cox JC, Reidel T;

WPI: 2002-090203/12.

Aptazyme construct for detecting the presence of ligands, comprises a regulatable Group I intron aptamer oligonucleotide with a regulatory domain, and modulates their kinetic parameters in response to an effector

Claim 10; Page 31; 42pp; English.

The sequence represents an oligonucleotide used in the invention in the construction of a group I regulatable aptazyme pool. The invention relates to a novel aptazyme construct comprising a regulatable Group I intron aptamer oligonucleotide sequence having an allosterically regulatable regulatory domain, where the kinetic parameters of the aptazyme on a target gene vary in response to the interaction of an allosteric effector molecule with the regulatory domain, and the intron splicing reaction occurs in vitro. The aptazyme is useful: (1) in assays to detect the presence of ligands or to detect activation of an aptazyme by an effector; (2) in the identification, isolation and enhancement of allosteric effectors and of the allosterically regulatable aptazymes with which they interact; (3) to activate or repress a reporter gene (e.g.

CC Luciferase) containing an engineered intron in response to an endogenous  
CC activator; and (4) to monitor intracellular levels of proteins or small  
CC molecules such as cyclic AMP.  
XX

Sequence 131 BP; 37 A; 32 C; 24 G; 36 T; 2 other;

Query Match

Best Local Similarity 97.3%; Score 127.4; DB 24; Length 131;  
Matches 128; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCTGAGTATAAGTGACTTATCTGATATCTATCTAAACGGGACCTCTAGTAGA 60  
DB 1 GCCTGAGTATAAGTGACTTATCTGATATCTATCTAAACGGGACCTCTAGTAGA 60  
QY 61 CAATCCCGTGTCTAAATTAATTAACGAGCATGCTTGTATGCGCTTGAGATTAATGCTTAC 120  
DB 61 CAATCCCGTGTCTAAATTAATTAACGAGCATGCTTGTATGCGCTTGAGATTAATGCTTAC 120  
QY 121 GACTATCCCTT 131  
DB 121 GACTATCCCTT 131

RESULT 6

AAL43050  
ID AAL43050 standard; DNA; 133 BP.

AC AAL43050;

DT 25-SEP-2002 (first entry)

DE Regulatable, catalytically active nucleic acid construction oligo #9.

KW Regulatable catalytically active nucleic acid; RCANA; ribozyme;

OS Synthetic.

XX WO200196559-A2.

XX 20-DEC-2001.

PF 14-JUN-2001; 2001WO-US19302.

PR 15-JUN-2000; 2000US-212097P.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L,  
PI Davidson E, Cox JC, Reidel T;

XX WPI; 2002-122216/16.

PS Example 5; Page 68; 126pp; English.  
XX  
CC The present invention relates to regulatable, catalytically active  
CC nucleic acids (RCANAs) which are regulated by polypeptides. These are  
CC useful for regulating gene expression, in assays for detecting the  
CC presence of ligands, for activation of an effector of RCANA, and in gene  
CC therapy. The present sequence is an oligonucleotide used in the  
CC construction of an RCANA.

XX  
XX Sequence 133 BP; 37 A; 33 C; 25 G; 38 T; 0 other;

Query Match

Best Local Similarity 83.2%; Score 109; DB 24; Length 133;  
Matches 131; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 GCCTGAGTATAAGTGACTTATCTGATATCTATCTAAACGGGACCTCTAGTAGA 60  
DB 1 GCCTGAGTATAAGTGACTTATCTGATATCTATCTAAACGGGACCTCTAGTAGA 60  
QY 61 CAATCCCGTGTCTAAATTAATTAACGAGCATGCTTGTATGCGCTTGAGATTAATGCTTAC 118  
DB 61 CAATCCCGTGTCTAAATTAATTAACGAGCATGCTTGTATGCGCTTGAGATTAATGCTTAC 120  
QY 119 AGCATATCCCTT 131  
DB 121 AGCATATCCCTT 133

RESULT 7

AAL43052  
ID AAL43052 standard; DNA; 129 BP.

AC AAL43052;

DT 25-SEP-2002 (first entry)

DE Regulatable, catalytically active nucleic acid construction oligo #11.

KW Regulatable catalytically active nucleic acid; RCANA; ribozyme;

OS Synthetic.

XX WO200196559-A2.

XX 20-DEC-2001.

PF 14-JUN-2001; 2001WO-US19302.

PR 15-JUN-2000; 2000US-212097P.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L,  
PI Davidson E, Cox JC, Reidel T;

XX WPI; 2002-122216/16.

PS New regulatable, catalytically active nucleic acids (RCANA), useful in  
PS gene therapy (particularly for regulating gene expression), or in  
PS assays for detecting the presence of ligands or activation of an  
PS effector of RCANA -  
XX Example 5; Page 68; 126pp; English.

XX  
CC The present invention relates to regulatable, catalytically active  
CC nucleic acids (RCANAs) which are regulated by polypeptides. These are  
CC useful for regulating gene expression, in assays for detecting the  
CC presence of ligands, for activation of an effector of RCANA, and in gene  
CC therapy. The present sequence is an oligonucleotide used in the  
CC construction of an RCANA.

XX  
XX Sequence 129 BP; 36 A; 32 C; 24 G; 37 T; 0 other;

Query Match  
Best Local Similarity 81.7%; Score 107; DB 24; Length 129;  
Matches 129; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 GCCTGAGTATAAGTGACTTATCTGATATCTATCTAAACGGGACCTCTAGTAGA 60  
DB 1 GCCTGAGTATAAGTGACTTATCTGATATCTATCTAAACGGGACCTCTAGTAGA 60  
QY 61 CAATCCCGTGTCTAAATTAATTAACGAGCATGCTTGTATGCGCTTGAGATTAATGCTTAC 120  
DB 61 CAATCCCGTGTCTAAATTAATTAACGAGCATGCTTGTATGCGCTTGAGATTAATGCTTAC 118  
QY 121 GACTATCCCTT 131  
DB 121 GACTATCCCTT 131



PR 15-JUN-2000; 2000US-212097P.  
XX (TEXA ) UNIV TEXAS SYSTEM.  
XX

PI Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L,  
PI Davidson E, Cox JC, Reidel T;  
XX WPI; 2002-122216/16;

DR New regulatable, catalytically active nucleic acids (RCANA), useful in  
XX gene therapy (particularly for regulating gene expression), or in  
XX assays for detecting the presence of ligands or activation of an  
XX effector of RCANA

PS Example 5; Page 68; 126pp; English.

CC The present invention relates to regulatable, catalytically active  
CC nucleic acids (RCANAs) which are regulated by polypeptides. These are  
CC useful for regulating gene expression, in assays for detecting the  
CC presence of ligands, for activation of an effector of RCANA, and in gene  
CC therapy. The present sequence is an oligonucleotide used in the  
CC construction of an RCANA.

XX Sequence 115 BP; 30 A; 30 C; 22 G; 33 T; 0 other;

Query Match 63.7%; Score 83.4; DB 24; Length 115;  
Best Local Similarity 91.9%; Pred. No. 1.2e-20;  
Matches 102; Conservative 0; Mismatches 1; Indels 8; Gaps 1;

OY 1 GCCGTGATTAAGGTGACTTATCTATCTATCTATCTAAGGGGAACTCTCTAGTACA 60

DB 1 GCCGTGATTAAGGTGACTTATCTATCTATCTAAGGGGAACTCTCTAGTACA 60

OY 61 CAATCCCGTCTAATTAATATACGACATCGCTTGATGCCCTGGACATAA 111

DB 61 CAATCCCGTCTAATTAATATACGACATCGCTTGATGCCCTGGACATAA 103

RESULT 11  
AAL43067

ID AAL43067 standard; RNA; 82 BP.

XX AAL43067;

DT 25-SEP-2002 (first entry)

XX Regulatable, catalytically active nucleic acid #2.

KW Regulatable catalytically active nucleic acid; RCANA; ribozyme;

XX gene therapy; ss.

XX Unidentified.

XX Key

FT misc\_binding

FT stem\_loop

FT misc\_binding

FT misc\_binding

FT misc\_binding

FT stem\_loop

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```

FT stem_loop      14..24    /*tag= b  

FT misc_binding   29..33    /*tag= c  

FT misc_binding   34..35    /bound_moiety= "binds nucleotides 8-4 of itself"  

FT misc_binding   41        /*tag= d  

FT misc_binding   41        /bound_moiety= "binds nucleotides 79-78 of itself"  

FT misc_binding   41        /*tag= e  

FT misc_binding   45..46    /bound_moiety= "binds nucleotide 72 of itself"  

FT misc_binding   48..62    /*tag= f  

FT stem_loop      48..62    /bound_moiety= "binds nucleotides 68-67 of itself"  

FT misc_binding   67..68    /*tag= g  

FT misc_binding   72        /*tag= h  

FT misc_binding   72        /bound_moiety= "binds nucleotides 46-45 of itself"  

FT misc_binding   78..79    /*tag= i  

FT misc_binding   78..79    /bound_moiety= "binds nucleotide 41 of itself"  

FT misc_binding   /tag= j  

FT misc_binding   /bound_moiety= "binds nucleotides 35-34 of itself"  

XX WO200196559-A2.  

XX PD 20-DEC-2001.  

XX PF 14-JUN-2001; 2001WO-US19302.  

XX PR 15-JUN-2000; 2000US-212097P.  

XX PA (TEXA ) UNIV TEXAS SYSTEM.  

XX PI Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L;  

XX PI Davidson E, Cox JC, Reidel T;  

XX DR WPI; 2002-122216/16.  

XX PT New regulatable, catalytically active nucleic acids (RCNAs), useful in  

XX PT gene therapy (particularly for regulating gene expression), or in  

XX PT assays for detecting the presence of ligands or activation of an  

XX PT effector of RCNA -  

XX PS Example 5; Fig 25B; 126pp; English.  

XX CC The present invention relates to regulatable, catalytically active  

XX CC nucleic acids (RCNAs) which are regulated by polypeptides. These are  

XX CC useful for regulating gene expression, in assays for detecting the  

XX CC presence of ligands, for activation of an effector of RCNA, and in gene  

XX CC therapy. The present sequence is an RCNA described in the  

XX CC exemplification of the invention.  

XX SQ Sequence 82 BP; 24 A; 21 C; 16 G; 21 U; 0 other:  

Query Match          62.6%; Score 82; DB 24; Length 82;  

Best Local Similarity 74.4%; Pred. No. 3.5e-20;  

Matches 61; Conservative 21; Mismatches 0; Indels 0; Gaps 0  

OY 37 TAACGGGGAACCTCTAGTACATCCCGTGCTAAATTATACGACATGCTTTGAT 96  

DB 1 UAACGGGGGAACCTCUCAGUAGACAACUCCGCCUGCAUAUADACGACHUGCUUGAU 60  

OY 97 GCCCTTGGCAGATAAATGCTTA 118  

DB 61 GCCCUDGGCAGUAUAUGCCTA 82
```

Accession	Entry	Location/Qualifiers
XX	ABN83051;	
AC		
XX	16-AUG-2002 (first entry)	
DT		
XX	GpITH1P6.131 aptamer construct.	
DE		
XX	Aptazyme; regulatable; aptamer; luciferase; cyclic AMP; ss;	
XX	GpITH1P6.131.	
KW		
XX	Unidentified.	
OS		
XX		
FH	Key	Location/Qualifiers
FT	misc_binding	4..9
FT		/*tag= a
FT		/bound_moiety= "Bases 33-28"
FT	stem_loop	14..24
FT		/*tag= b
FT		28..33
FT	misc_binding	/*tag= c
FT		/bound_moiety= "Bases 9-4"
FT		34..35
FT	misc_binding	/*tag= c
FT		/bound_moiety= "Bases 79-78"
FT		41
FT	misc_binding	/*tag= d
FT		/bound_moiety= "Base 72"
FT		45..46
FT	misc_binding	/*tag= e
FT		/bound_moiety= "Bases 68-67"
FT	stem_loop	48..62
FT		/*tag= f
FT		67..68
FT	misc_binding	/*tag= g
FT		/bound_moiety= "Bases 46-45"
FT		72
FT	misc_binding	/*tag= h
FT		/bound_moiety= "Base 41"
FT		78..79
FT	misc_binding	/*tag= i
FT		/bound_moiety= "Bases 35-34"
XX		
XX	WO200196541-A2.	
PN		
PD	20-DEC-2001.	
XX		
XX	15-JUN-2001; 2001WO-US19119.	
PF		
XX		
XX	15-JUN-2000; 2000US-0661658.	
PR		
XX		
PA	(TEXAS) UNIV TEXAS.	
XX		
XX	Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L,	
PI	Davidson E, Cox JC, Reidel T;	
PI		
XX	WPI; 2002-090203/12.	
DR		
XX		
XX	Aptazyme construct for detecting the presence of ligands, comprises a	
PT	regulatable group I intron aptamer oligonucleotide with a regulatory	
PT	domain, and modulates their kinetic parameters in response to an	
PT	effector	
PS		
XX	Disclosure; Fig 2A; 42pp; English.	
XX		
CC	The sequence represents the GpITH1P6.131 aptamer construct used in the	
CC	invention. The invention relates to a novel aptazyme construct comprising	
CC	a regulatable group I intron aptamer oligonucleotide sequence having an	
CC	allosterically regulatable regulatory domain, where the kinetic	
CC	parameters of the aptazyme on a target gene vary in response to the	
CC	interaction of an allosteric effector molecule with the regulatory	
CC	domain, and the intron splicing reaction occurs in vitro. The aptazyme is	
CC	useful: (1) in assays to detect the presence of ligands or to detect	
CC	activation of an aptazyme by an effector; (2) in the identification,	

CC Isolation and enhancement of allosteric effectors and of the  
 CC allosterically regulatable aptazymes with which they interact; (3) to  
 CC activate or repress a reporter gene (e.g. luciferase) containing an  
 CC engineered intron in response to an endogenous activator; and (4) to  
 CC monitor intracellular levels of proteins or small molecules such as  
 CC cyclic AMP.

SO Sequence 82 BP; 24 A; 21 C; 16 G; 21 U; 0 other;

Query Match 62.6%; Score 82; DB 24; Length 82;  
 Best Local Similarity 74.4%; Pred. No. 3.3e-20;  
 Matches 61; Conservative 21; Mismatches 0; Indels 0; Gaps 0;

QY 37 TAAACGGGGAACCTCTCTAGTACATCCGCTAAATTAACGACGATGCTGTGAT 96  
 Db 1 UAAACGGGGAACCTCTCTAGTACATCCGCTAAATTAACGACGATGCTGTGAT 96  
 QY 97 GCCCTTGGCAGATAAATGGCTA 118  
 Db 61 GCCCTTGGCAGATAAATGGCTA 82

# RESULT 14

AL43058  
 ID AAL43058 standard; DNA; 107 BP.

AC AAL43058;

DT 25-SEP-2002 (first entry)

DE Regulatable, catalytically active nucleic acid construction oligo #16.

KW Regulatable catalytically active nucleic acid; RCANA; ribozyme;

OS Synthetic.

PN WO200196559-A2.

PD 20-DEC-2001.

PF 14-JUN-2001; 2001WO-US19302.

PR 15-JUN-2000; 2000US-212097P.

PS (TEXA) UNIV TEXAS SYSTEM.

PI Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L;  
 Davidson E, Cox JC, Reidel T;

DR WPI; 2002-122216/16.

PT New regulatable, catalytically active nucleic acids (RCANA), useful in  
 PT gene therapy (particularly for regulating gene expression), or in  
 PT assays for detecting the presence of ligands or activation of an  
 PT effector of RCANA

PS Example 5; Page 69; 126pp; English.

CC The present invention relates to regulatable, catalytically active  
 CC nucleic acids (RCANAs) which are regulated by polypeptides. These are  
 CC useful for regulating gene expression, in assays for detecting the  
 CC presence of ligands, for activation of an effector of RCANA, and in gene  
 CC therapy. The present sequence is an oligonucleotide used in the  
 CC construction of an RCANA.

SO Sequence 107 BP; 31 A; 28 C; 19 G; 29 T; 0 other;

Query Match 62.1%; Score 81.4; DB 24; Length 107;  
 Best Local Similarity 97.2%; Pred. No. 6.3e-20;  
 Matches 104; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 27 GTAATCTATTAACGGGGAACCTCTCTAGTACATCCGCTAAATTAACGACG 85

Db 1 GTAAATCTATTAACGGGGAACCTCTCTAGTACATCCGCTAAATTAACGACG 60  
 QY 86 ATGCTCTTGAATGCGCTTGGCAG-ATAAATGCTTAACGACGATGCCCTT 131  
 Db 61 ATGCTCTTGAATGCGCTTGGCAGATAAATGCTTAACGACGATGCCCTT 107

# RESULT 15

AL43044  
 ID AAL43044 standard; DNA; 122 BP.

AC AAL43044;

DT 25-SEP-2002 (first entry)

DE Regulatable, catalytically active nucleic acid construction oligo #5.

KW Regulatable catalytically active nucleic acid; RCANA; ribozyme;

OS Synthetic.

PN WO200196559-A2.

PD 20-DEC-2001.

PF 14-JUN-2001; 2001WO-US19302.

PR 15-JUN-2000; 2000US-212097P.

PS (TEXA) UNIV TEXAS SYSTEM.

PI Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L;  
 Davidson E, Cox JC, Reidel T;

DR WPI; 2002-122216/16.

PT New regulatable, catalytically active nucleic acids (RCANA), useful in  
 PT gene therapy (particularly for regulating gene expression), or in  
 PT assays for detecting the presence of ligands or activation of an  
 PT effector of RCANA

PS Example 5; Page 67; 126pp; English.

CC The present invention relates to regulatable, catalytically active  
 CC nucleic acids (RCANAs) which are regulated by polypeptides. These are  
 CC useful for regulating gene expression, in assays for detecting the  
 CC presence of ligands, for activation of an effector of RCANA, and in gene  
 CC therapy. The present sequence is an oligonucleotide used in the  
 CC construction of an RCANA.

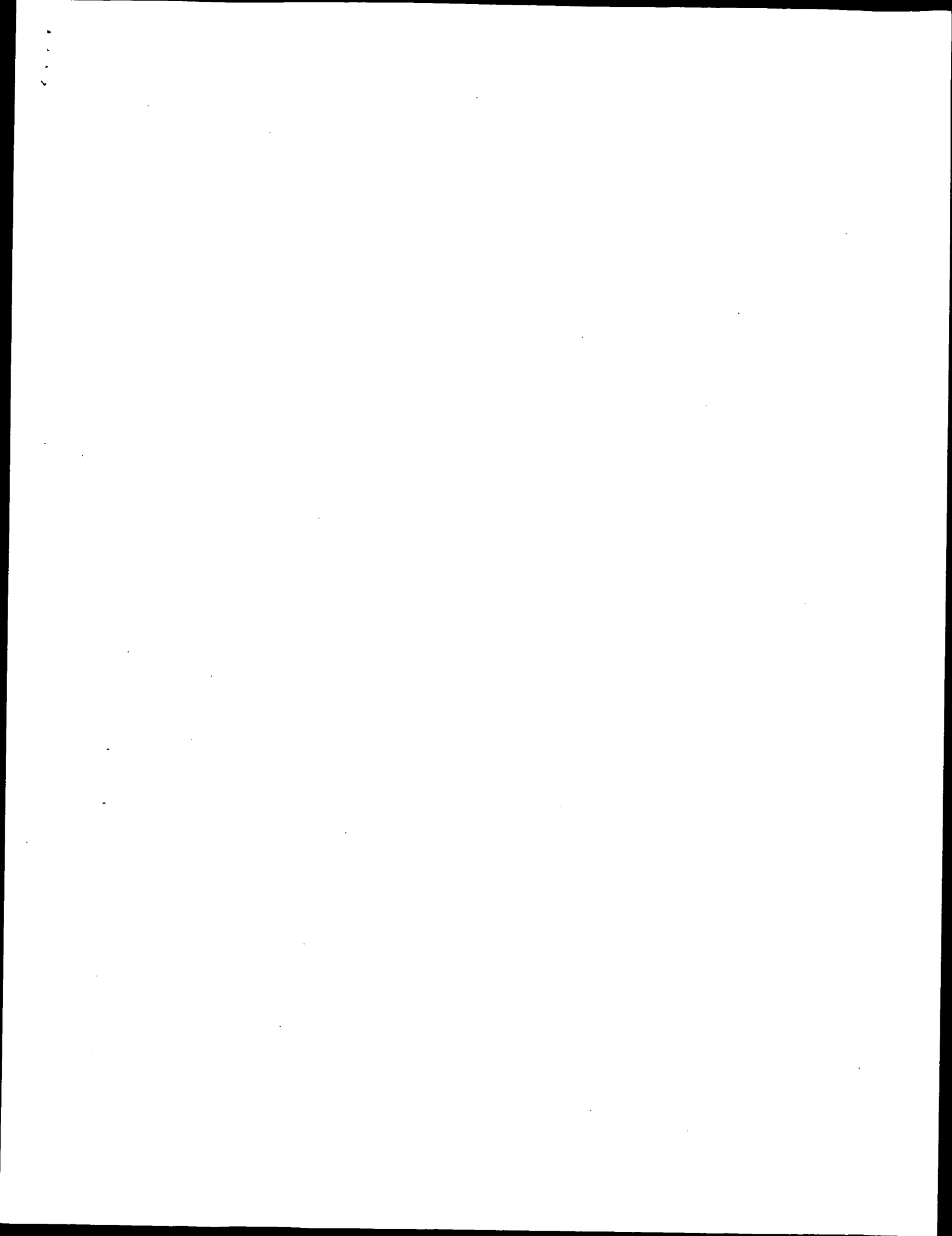
SO Sequence 122 BP; 34 A; 29 C; 24 G; 35 T; 0 other;

Query Match 61.5%; Score 80.6; DB 24; Length 122;  
 Best Local Similarity 82.4%; Pred. No. 1.3e-19;  
 Matches 108; Conservative 0; Mismatches 14; Indels 9; Gaps 1;

QY 1 GCCTAGCTAATGAGGACTATCTTGAATCTAATTAACGGGGAACCTCTAGTACA 60  
 Db 1 GCCTAGCTAATGAGGACTATCTTGAATCTAATTAACGGGGAACCTCTAGTACA 60  
 QY 61 CAATCCCGCTTAATTAATTAACGACGATGCTGTATGCCCTTGGCAGATAAATGCCCTAAC 120  
 Db 61 CAATCCCGCTTAATTAATTAACGACGATGCTGTATGCCCTTGGCAGATAAATGCCCTAAC 120  
 QY 121 GACTATCCCTT 131  
 Db 112 GACTATCCCTT 122

Search completed: July 13, 2003, 22:15:21  
 Job time: 149 secs







GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 13, 2003, 21:34:47 ; Search time 1135 Seconds  
(without alignments)  
1869.259 Million cell updates/sec

Title: US-09-661-658b-2

Perfect score: 131  
Sequence: 1 gcctagagataagtgactt.....atgcctaacgataccctt 131

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues  
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: em\_estb1:\*  
2: em\_estb1:\*  
3: em\_estb1:\*  
4: em\_estb1:\*  
5: em\_estb1:\*  
6: em\_estb1:\*  
7: em\_estb1:\*  
8: em\_estb1:\*  
9: gb\_est1:\*  
10: gb\_est1:\*  
11: gb\_est1:\*  
12: gb\_est1:\*  
13: gb\_est1:\*  
14: gb\_est1:\*  
15: em\_estb1:\*  
16: em\_estb1:\*  
17: gb\_est1:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_hum:\*  
20: em\_gss\_hum:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_vrt:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mam:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	32.8	25.0	525	17 BH280107	BH280107 CH230-117
2	31.6	24.1	443	10 AW989880	AW989880 u19h10.Y
3	31.6	24.1	1068	11 AK017255	AK017255 Mus muscu
4	31.2	23.8	682	17 BH245494	BH245494 PSB0764 S
5	31	23.7	570	17 AQ060314	AQ060314 CIT-HSP-2
6	30.8	23.5	340	17 AZ489123	AZ489123 1M0319E14

7	30.6	23.4	1004	17 CNS049YL	AL281190 Tetraodon
8	30	22.9	584	17 AZ742331	AZ742331 RPI-24-6
9	29.6	22.6	601	17 AQ461684	AQ461684 HS_5208-A
10	29.4	22.4	268	17 AQ239325	AQ239325 RPI-11-68
11	29.4	22.4	492	14 L26622	L26622 MUSH033A.1a
12	29.4	22.4	565	17 AQ628517	AQ628517 CTBT-E1-
13	29.2	22.3	371	14 D63293	D63293 HUM519C108
14	29	22.1	414	14 BQ634483	BQ634483 NKX069_E
15	29	22.1	545	17 AZ159311	AZ159311 SP_0062-B
16	29	22.0	568	9 AT655148	AT655148 u10309.Y
17	28.8	22.0	451	17 BH732140	BH732140 BOMB64TF
18	28.8	22.0	1029	17 CINS05LK5	AL342878 Tetraodon
19	28.6	21.8	281	17 BH158201	BH158201 BH158201
20	28.6	21.8	500	17 BH4840744	BH4840744 K607177-3
21	28.6	21.8	620	17 BH126169	BH126169 RPI-24-2
22	28.6	21.8	803	17 AQ030012	AQ030012 Pan trogl
23	28.4	21.7	150	9 AA382203	AA382203 EST95373
24	28.4	21.7	491	17 AZ031655	AZ031655 RPI-23-2
25	28.4	21.7	560	17 AQ0601442	AQ0601442 HS_2096.A
26	28.4	21.7	563	17 BH464962	BH464962 BOCG377E
27	28.4	21.7	638	12 BF647865	BF647865 NF038A09E
28	28.4	21.7	674	17 BH531194	BH531194 BOCG590TR
29	28.4	21.7	882	12 BP120755	BP120755 601758145
30	28.4	21.7	868	17 CINS03609	AL243234 Tetraodon
31	28.4	21.7	1029	17 CINS01X05	AL172166 Tetraodon
32	28.2	21.5	386	10 AV936181	AV936181 AV936181
33	28.2	21.5	399	13 BJ276119	BJ276119 BJ276119
34	28.2	21.5	428	14 BQ788526	BQ788526 WTJ19 whe
35	28.2	21.5	458	14 BQ243052	BQ243052 Tael15019G
36	28.2	21.5	479	13 BG945339	BG945339 PMO-AN08
37	28.2	21.5	480	9 AL499891	AL499891 AL499891
38	28.2	21.5	619	14 BQ619850	BQ619850 Tair1151A
39	28.2	21.5	639	10 BE566390	BE566390 601339986
40	28.2	21.5	672	13 BJ253216	BJ253216 BJ253216
41	28.2	21.5	709	6 BQ238482	BQ238482 TAE05003P
42	28.2	21.5	712	13 BJ311709	BJ311709 BJ311709
43	28.2	21.5	755	12 BF184543	BF184543 601842850
44	28.2	21.5	835	17 AZ544758	AZ544758 ENTF94TR
45	28	21.4	377	14 C66385	C66385 C66385 YUJ1

## ALIGNMENTS

RESULT 1  
LOCUS BH280107  
DEFINITION CH230-117E23, TV CHORI-230 Segment 1 Rattus norvegicus genomic clone  
ACCESSION BH280107  
VERSION BH280107.1  
KEYWORDS GI:1192509  
SOURCE GSS.  
ORGANISM Norway rat.  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 525)  
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn  
,A., Gebregeorgis,E., Overton,U., Russell,D., Chen,D., Riggs,F., de  
Jong,P. and Fraser,C.M.  
Rat BAC End Sequences from Library CHORI-230 EcORI segment  
Unpublished (1999)  
Other-GSS: CH230-117E23.TV  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the rat BAC library CHORI-230  
(http://www.chori.org/bacpac/rat230.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cbo.org).

Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/or erting\_information.htm). BAC end  
page: http://www.tigr.org/tdb/bac\_ends/rat/bac\_end\_intro.html  
Plate: 117 row: E column: 23

Seq primer: Sp6

Class: BAC ends.

Location/Qualifiers

1. 525

/organism="Rattus norvegicus"

/strain="BN/SSNhd/MCW"

/db\_xref="taxon:10116"

/clone="CH230-117E23"

/clone\_lib="CHORI-230 Segment 1"

/sex="Female"

/cell\_type="Brain"

/note="Vector: PTAHBAC2.1; Site:1: EcoRI; Site:2: EcoRI;

CHORI-230 Rat (BN/SSNhd/MCW) BAC library produced by

Pieter de Jong"

BASE COUNT 165 a 88 c 86 g 186 t

ORIGIN

Query Match 25.0%; Score 32.8; DB 17; Length 525;

Best Local Similarity 59.8%; Pred. No. 1.7;

Matches 55; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

4 TGAGTATAGTACTTACTTCTAATCTAATAAGGAGGACCTCTAGTACAA 63

44 TCTGTGTAGGCTCTTTTCTGATCTCTAATCAGAGATTTCATAGTACAA 103

64 TCCCGTGTCTAATTTATACAGCATGCTGTGA 95

104 TCTTGAGCACACACTACAAATATGTTT 135

RESULT 2

AW989880/c 443 bp mRNA linear EST 02-JUN-2000

LOCUS u19h10.y1 Soares\_mammary\_gland\_MMLG Mus musculus cDNA clone

DEFINITION IMAGE:1511875 5', mRNA sequence.

ACCESSION AW989880

VERSION AW989880.1 GI:8185380

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

1 (bases 1 to 443)

NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

This clone is available royalty-free through LINL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

MGI:938727

Seq primer: 40RP from Gibco.

Location/Qualifiers

1. 443

/organism="Mus musculus"

/db\_xref="taxon:10090"

/clone="IMAGE:1511875"

/clone\_lib="Soares\_mammary\_gland\_MMLG"

/sex="female (lactating)"

/tissue\_type="mammary gland"

/lab\_host="DH10B"

/note="Vector: pRTT3-Pac (Pharmacia) with a modified

polylinker. 1st strand cDNA was prepared from mammary

gland tissue from a lactating female, and was then primed

with a Not I - oligo(dT) primer. Double-stranded cDNA was

ligated to Eco RI adaptors (Pharmacia), digested with Not

I and cloned into the Not I and Eco RI sites of the

modified pT773 vector. Library is normalized. Library  
was constructed by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 125 a 95 c 115 g 108 t

ORIGIN

Query Match 24.1%; Score 31.6; DB 10; Length 443;

Best Local Similarity 60.5%; Pred. No. 4;

Matches 52; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

1 GCCTGAGTATAGGCTGCTTATCTGATCTAATCTAAGGAGGACCTCTAGTACA 60

314 GCTTGTAGTACACTTTCATATCCATAGTTCAGACACAGAAAATCTCCAGCCGA 255

61 CAATCCCGCTGCTAATATATCCAGCA 86

254 GACCGCGCTGCTAGGCTACCTCGAA 229

Db

RESULT 3

AK017255/c 1068 bp mRNA linear HTC 19-JAN-2002

LOCUS AK017255

DEFINITION Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched

library, clone:5430401H09;hypothetical protein, full insert

sequence.

ACCESSION AK017255

VERSION AK017255.1 GI:12856401

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (strain:C57Bl/6J) 6 days neonate head cDNA to mRNA,

clone:lib:RIKEN full-length enriched mouse cDNA library

clone:5430401H09.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

10349636

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subcloning of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

11042159

3

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

Konno, H., Akiyama, J., Nishi, K., Katsuna, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multiplexed sequencing

genome Res. 10 (11), 1757-1771 (2000)

20530913

11076861

4

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,

Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,

Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, J., Yamanaka, I.,

Saito, T., Okazaki, Y., Gotohori, T., Bono, H., Kasukawa, T., Saito, R.,

Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,

Fleischmann, W., Gaasterland, T., Gissi, C., King, J., Kociba, H.,

Kuvel, P., Lewis, S., Matsuno, Y., Niki, C., Pesole, G.,

Quackenbush, J., Schriml, L.M., Staahl, F., Suzuki, R., Tomita, M.,

Wagner, L., Washio, T., Sakai, K., Okita, T., Furuno, M., Aono, H.,

Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,

Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,

Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,



ACCESSION A0060314  
 VERSION A0060314.1 GI:3362567  
 KEYWORDS GSS.  
 SOURCE human.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 570)  
 Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,  
 Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,  
 Simon,M., and Venter,J.C.  
 Use of a random BAC end sequence database for sequence-ready map  
 building (1998)

## TITLE

JOURNAL Unpublished (1998)

## COMMENT

Contact: Mark Adams  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: mdamas@tigr.org  
 Clones are available from Research Genetics (info@resgen.com). BAC  
 end search page:  
[http://www.tigr.org/tdb/humgen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html).  
 Seq primer: M13 Reverse  
 Class: BAC ends.

## FEATURES

Location/Qualifiers

1..570  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="235103"  
 /clone\_id="CIT-HSP"  
 /sex="Male"  
 /cell\_type="Sperm"  
 /note="Vector: pBelBAC11; site\_1: HindIII; site\_2:  
 HindIII"

BASE COUNT 122 a 101 c 120 g 227 t

## ORIGIN

Query Match 23.7%; Score 31; DB 17; Length 570;  
 Best Local Similarity 62.0%; Pred. No. 7.1;  
 Matches 49; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 10 TAAGTGACTTACTTGAATCTATCTAAACGGGACCTCTAGTACATCCCGT 69  
 DB 375 TCAATGTTATTTATGCTTAAATCTGTTATGCGTGTATCATTTATGCTTCATAT 434  
 QY 70 GCTAATTTATACCATC 88  
 DB 435 GTTAACCTATCCCTGCATC 453

RESULT 6  
 A2489123 340 bp DNA linear GSS 05-OCT-2000  
 LOCUS 1M0319E14R Mouse 10kb plasmid UNGCJM library Mus musculus genomic  
 ACCESSION A2489123  
 VERSION A2489123  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 340)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,  
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
 and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss

University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0319 row: E column: 14  
 Seq primer: CACACGAGAAACACACTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 340.  
 Location/Qualifiers  
 1..340  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UNGCM0319E14"  
 /clone\_id="UNGCM0319E14"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

## FEATURES

## source

BASE COUNT 105 a 66 c 34 g 135 t

## ORIGIN

Query Match 23.5%; Score 30.8; DB 17; Length 340;  
 Best Local Similarity 58.9%; Pred. No. 6.5;  
 Matches 53; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 21 ATACTGTATCTATCTAAACGGGACCTCTAGTACATCCCGTAAATTATA 80  
 DB 165 ATATCTTATCTATCTAAATGTTACCTTTCCAGAGGCTGCTTTTCCATCATC 224  
 QY 81 CCAGCATCGCTTGATGCGCTTGCGAGATA 110  
 DB 225 CAACTCTTGTGTTTACTCTCTTGGAAGAA 254

RESULT 7  
 CNS049YL 1004 bp DNA linear GSS 21-MAY-2000  
 LOCUS 094B11 of library G from Tetradon nigroviridis, genomic survey  
 DEFINITION Tetradon nigroviridis genome survey sequence 17 end of clone  
 sequence.  
 ACCESSION AL281190.1 GI:8019499  
 VERSION AL281190.1  
 KEYWORDS GSS: genome survey sequence.  
 SOURCE Tetradon nigroviridis.  
 ORGANISM Tetradon nigroviridis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 Tetraodontidae; Tetraodon.  
 REFERENCE 1 (bases 1 to 1004)  
 Roest-Crolius,H., Tallon,O., Dasilva,C., Bouneau,L., Fisher,C.,

Libidly available at <http://www.chori.org/bacpac/orderingframe.htm>. Clones may be purchased from [pedejong@mail.choi.org](mailto:pedejong@mail.choi.org). BAC Resources (<http://www.chori.org/bacpac/orderingframe.htm>).

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="RPCI-11 Human Male BAC Library"  
 /sex="Male"  
 /note="Vector: pBAC3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
 Male blood DNA was isolated from one randomly chosen donor  
 and partially digested with a combination of EcoRI and  
 EcoRI Methylase. Size selected DNA was cloned into the  
 pBAC3.6 vector at EcoRI sites"

BASE COUNT 165 a 129 c 105 g 185 t 17 others  
 ORIGIN

Query Match 22.6%; Score 29.6; DB 17; Length 601;  
 Best Local Similarity 59.5%; Pred. No. 22;  
 Matches 50; Conservative 0; Mismatches 34; Indels 0; Gaps 0;  
 QY 15 TGACTTATCTTATCTATCTAAACGGGACCTCTGTAGACATCCGCTGTA 74  
 Db 260 TAACTCATGTGCAACCAATCTAATTGGGAACATCTGTATAGACTGTCTCTGTG 319  
 QY 75 ATTATACCAACATCTGTGATGC 98  
 Db 320 AATAGACATGATCTTACTTCAATTC 343

RESULT 10  
 AO239325 268 bp DNA linear GSS 21-APR-1999  
 LOCUS RPCI11-68A11.TK RPCI-11 Homo sapiens genomic clone RPCI-11-68A11,  
 DEFINITION DNA sequence.  
 ACCESSION AO239325  
 VERSION AO239325.1 GI:3671616  
 KEYWORDS GSS.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 1 (bases 1 to 268)  
 Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,  
 Berry, K., Granger, D., Sun, E., Wible, C., de Jong, P. and Venter, J.C.  
 Use of human BAC End Sequences for Sequence-Ready Map Building  
 Unpublished (1998)  
 Other GSS: RPCI11-68A11.TU  
 Contact: Mark Adams  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0208  
 Fax: 301 838 0208  
 Email: mdadams@igf.org

Clones are derived from the human BAC library RPCI-11. For BAC  
 library availability, please contact Pieter de Jong  
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from  
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from  
 Research Genetics (info@resgen.com). BAC end search page:  
 http://www.tigr.org/tdb/hungen/bac\_end\_search/bac\_end\_search.html  
 Seg primer: 17  
 Class: BAC ends.

FEATURES  
 source  
 1. 268  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="GDB:7525738"  
 /db\_xref="taxon:9606"  
 /clone\_lib="RPCI-11-68A11"  
 /clone\_lib="RPCI-11"  
 /sex="Male"  
 /cell\_type="Lymphocytes"  
 /note="Vector: pBAC3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
 Male blood DNA was isolated from one randomly chosen donor  
 and partially digested with a combination of EcoRI and  
 EcoRI Methylase. Size selected DNA was cloned into the  
 pBAC3.6 vector at EcoRI sites"  
 RPCI11 Human Male BAC Library"  
 BASE COUNT 92 a 37 c 41 g 97 t 1 others  
 ORIGIN

Query Match 22.4%; Score 29.4; DB 17; Length 268;  
 Best Local Similarity 54.8%; Pred. No. 18;  
 Matches 57; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 GGCTAGATTAAGTGAAGTAACTTATCTATCTATCTAAACGGGACCTCTAGTAGA 60  
 Db 24 GGCTAGATTAAGTGAAGTAACTTATCTATCTATCTAAACGGGACCTCTAGTAGA 60  
 QY 61 CAATCCGCTGCTAATTAATTAACGCAATGCTTGAATGCCCTTG 104  
 Db 84 CAACTCCTAGAAAATCATCTGTTGTTTGTGTTGCTTG 127

RESULT 11  
 L26622/c 492 bp mRNA linear EST 01-MAR-1995  
 LOCUS MUSB033A lambda unizap male testis Mus musculus CDNA clone B033,  
 DEFINITION mRNA sequence.  
 ACCESSION L26622  
 VERSION L26622.1 GI:437412  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 1 (bases 1 to 492)  
 Kerr, S.M., Vambrie, S., McKay, S.J. and Cooke, H.J.  
 Analysis of cDNA sequences from mouse testis  
 Mamm. Genome 5, 557-565 (1994)  
 95093181  
 Contact: Kerr, S.M., Vambrie, S., McKay, S.J. and Cooke, H.J.

FEATURES  
 source  
 1. 492  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /strain="Swiss"  
 /db\_xref="taxon:10090"  
 /clone\_lib="B033"  
 /clone\_lib="lambda unizap male testis"  
 /note="Vector: lambda unizap; lambda unizap library from  
 male mouse testis"  
 BASE COUNT 181 a 87 c 69 g 150 t 5 others  
 ORIGIN

Query Match 22.4%; Score 29.4; DB 14; Length 492;  
 Best Local Similarity 60.8%; Pred. No. 23;  
 Matches 48; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 34 ATCTAAACGGGGAACCTCTCTAGTACACATCCGCTGCTAATTAATTAACGATCGTCTT 93  
 Db 79 ATCTGAATGGAAGAAACGACGATGACCATTCACACCTAGCAATGCTCTCTGTGAA 20  
 QY 94 GATCCCTTGGCGAGATAA 112  
 Db 19 ATTCCCTTGGCGAGATCA 1

RESULT 12  
 AO628517/c 565 bp DNA linear GSS 16-JUN-1999  
 LOCUS CITBI-El-2653612.TF CITBI-El Homo sapiens genomic clone 2653612,  
 DEFINITION DNA sequence.  
 ACCESSION AO628517  
 VERSION AO628517.1 GI:5090909  
 KEYWORDS GSS.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 1 (bases 1 to 565)  
 Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and  
 Venter, J.C.  
 Use of BAC End Sequences from Caltech Libraries for Sequence-Ready  
 Map Building



```

DEFINITION  SP_0062.B1.B1_77A Strongylocentrotus purpuratus, purple sea urchin
              , sperm genomic BAC library Strongylocentrotus purpuratus genomic
              clone Plate-62 Col-21 Row-D, DNA sequence.
ACCESSION   AZ159311
VERSION     AZ159311.1 GI:8311927
KEYWORDS    GSS.
SOURCE      Strongylocentrotus purpuratus.
ORGANISM    Strongylocentrotus purpuratus
            Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
            Echinoidea; Euechinoidea; Echinacea; Echinoida;
            Strongylocentrotidae; Strongylocentrotus.
REFERENCE   1 (bases 1 to 545)
            Cameron,R.A., Mahaltras,G., Rast,J.P., Martinez,P., Biondi,T.R.,
            Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray,
            ,G.A., Eitensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and
            Hood,L.
            A sea urchin genome project: Sequence scan, virtual map, and
            additional resources
            Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
JOURNAL     20402566
MEDLINE
COMMENT     Contact: Cameron, RA, Davidson, EH, Hood, L
            Division of Biology 156-29
            California Institute of Technology
            Pasadena California 91125, USA
            Tel: (626) 395-8421
            Fax: (626) 793-3047
            Email: acameron@caltech.edu
            Plate: 62 row: D column: 21
            Seq primer: T7
            Class: BAC ends
            High quality sequence stop: 545.
            Location/Qualifiers
              1..545
                /organism="Strongylocentrotus purpuratus"
                /db_xref="taxon:7668"
                /clone="Plate-62 Col=21 Row=D"
                /clone_lib="Strongylocentrotus purpuratus, purple sea
                urchin, sperm genomic BAC library"
                /note="Organ: sperm; Vector: BAC3.6; BAC clones in E-Coli
                DH10B"
BASE COUNT  151 a      86 c      116 g      177 t      15 others
ORIGIN
Query Match      22.1%; Score 29; DB 17; Length 545;
Best Local Similarity 58.8%; Pred. No. 33;
Matches 50; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 4 TGAGTATAGGTGACTTACTTGTATCTAATCTAATACGGGAGACTCTCTAGTAGCA 63
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 453 TGAAGTTATGGAGATGATATTTTATATATCTGAAGCTGGAGCCTCTAGCATAAATGG 512
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 64 TCCCGTCTAATAATTATACGACATC 88
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 513 TCCCATTTCTTCATTTTCTTAGCTTC 537
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Search completed: July 13, 2003, 22:35:19  
 Job time : 1140 secs



Gencore version 5.1.6  
1993 - 2003 CompuGen Ltd.

307

OM nucleic - nucleic search, using SW model  
 July 13, 2003, 18:59:57 : Search time 37 seconds  
 (without alignments) updates/sec  
 1085.802 Million cell

Run on

US-09-661-658B-2

Title score:	131
perfect sequence:	1 gcctgagtataagtgacc
Sequence:	
	IDENTITY-NUC Gapext 1.0

Scoring table: Gapop 10.0 , 153338381 residues

441362 seqs, 15333000  
-parameters: 882/24

Searched:

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Total number: 0
length: 0
```

Minimum DB	seq length	Match 0%
Maximum		Match 100%

	Maximum	Maximum
Listing first	45	summaries
post-processing		

Contents: NA: \*  
COMB. seq: \*

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Database :
Issued_patents_inr:
1: /cgn2-6/ptodata/1/ina/5A-COMB.seq: *
2: /cgn2-6/ptodata/1/ina/5B-COMB.seq: *
3: /cgn2-6/ptodata/1/ina/6A-COMB.seq: *
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6: /cgn2_6/ptodata/1/lna/backfiles.r.o.

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Pred. No. is greater than or equal to the total score greater by analysis of the total score and is derived by analysis of the total score

SUMMARIES

## SUMMARIES

Description

Result No.	Score	Query Match	Length	DB	LP	Sequence
1	78.4	59.8	510	1	US-08-431-896B-1	Sequence 30, Appl
2	37.2	28.4	59	4	US-09-257-503A-30	Sequence 24, Appl
3	37.2	28.4	123	4	US-09-257-503A-29	Sequence 27, Appl
4	37.2	28.4	125	4	US-09-257-503A-27	Sequence 28, Appl
5	37.2	28.4	149	4	US-09-257-503A-28	Sequence 29, Appl
6	37.2	28.4	142	1	US-08-443-957-29	Sequence 37, Appl
7	37.2	28.4	38	1	US-08-443-957-37	Sequence 6, Appl
8	30.4	23.2	40	1	US-08-443-957-6	Sequence 20, Appl
9	28.4	21.7	5140	3	US-08-825-852-20	Sequence 1, Appl
10	28.4	21.7	5140	4	US-09-032-888-20	Sequence 1, Appl
11	28.4	21.7	6127	2	US-09-032-352B-1	Sequence 1, Appl
12	28.4	21.7	6127	4	US-09-087-207C-1	Sequence 89, Appl
13	28.4	21.7	6127	4	US-09-100-005-1	Sequence 5, Appl
14	27.4	20.9	6127	2	US-08-226-819-89	Sequence 33, Appl
15	27.4	20.9	1185	1	US-08-458-638-5	Sequence 9, Appl
16	26	19.8	559	1	US-08-459-503A-33	Sequence 4, Appl
17	25.2	19.2	1558	1	US-09-257-503A-33	Sequence 4, Appl
18	25.2	19.2	1886	1	US-07-891-942G-7	Sequence 12, Appl
19	25.2	19.2	1920	1	US-07-891-942G-9	Sequence 12, Appl
20	25.2	19.2	43676	3	US-07-891-942G-9	Sequence 12, Appl
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22	24.6	18.8	8220	2	US-09-056-01-077-19	Sequence 11, Appl
23	24.6	18.8	8220	2	US-09-221-0178-11	Sequence 11, Appl
24	24.6	18.8	8220	2	US-08-568-439A-11	Sequence 11, Appl
25	24.6	18.8	8220	2	US-08-487-826B-11	Sequence 11, Appl
26	24.6	18.8	19124	4	US-09-210-268-1	Sequence 11, Appl
27	24.4	18.6	1789	2	US-08-487-826B-13	Sequence 11, Appl
					US-08-455-543A-29	Sequence 29, Appl

28	24.4	18.6	1789	2	US-08-223-305C-29
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ALIGNMENTS

## ALIGNMENTS

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Sequence 3, Appl  
Sequence 3, Appl  
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Sequence 766, App  
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Sequence 2, Appl  
Sequence 89, Appl  
Sequence 9, Appl  
Sequence 10, Appl  
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Sequence 10, Appl  
Sequence 6, Appl
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RESULT 1  
 US-08-431-8968-1 Application US/084318968  
 Sequence 1, 5773244  
 Patent No.: Information:  
 GENERAL APPLICANT: Ares, Manuel, Jr.  
 APPLICANT: Ford, Ethan E.  
 APPLICANT: RNA Cyclase Ribozymes  
 TITLE OF INVENTION: 7  
 NUMBER OF SEQUENCE: 7  
 CORRESPONDENCE ADDRESS: Townsend and Townsend and Crew LLP  
 ADDRESSEE: Townscenter Center, Eighth Floor  
 STREET: Two Emancipo  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: US8934  
 ZIP: 94111-8968  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: IBM PC compatible  
 COMPUTER: SYSTEM: PC-DOS/MS-DOS  
 OPERATING: PatentIn Release #1.0, Version #1.30  
 SOFTWARE: APPLICATION DATA: /08/431.8968  
 CURRENT APPLICATION NUMBER: US-08-431-8968  
 FILING DATE: 01-MAY-1995  
 APPLICATION NUMBER: 435  
 FILING LOCATION: 435  
 CLASSIFICATION DATA: US 08/063,857  
 PRIOR APPLICATION NUMBER: 19-1993  
 FILING DATE: 19-MAY-1993  
 FILING AGENT INFORMATION:  
 ATTORNEY/Weber, Kenneth A.  
 NAME: REGISTRATION NUMBER: 31,677  
 REFERENCE/DOCKET INFORMATION: 02307E-070000US  
 TELECOMMUNICATION NUMBER: 415 576-0300  
 TELEPHONE: (415) 576-0300  
 TELEFAX: (415) ID NO: 1  
 INFORMATION FOR SEQ: 1  
 INFORMATION CHARACTERISTICS:  
 SEQUENCE LENGTH: 510 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
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Tue Jul 15 10:33:02 2003

us-09-661-658b-2.rni

Page 2

Db 341 GCCUGAGUAAAGUGACUUAUACUCUUAUACUUAACGAGGAGACCCUCUCUAGUAGA 400  
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US-09-257-503A-30  
Sequence 30, Application US/09257503A  
Patent No. 6387617  
GENERAL INFORMATION:  
APPLICANT: ASHER, Nathan  
APPLICANT: ELKHOCHINSKY, Yaron  
FILE REFERENCE: ASHER-2  
CURRENT APPLICATION NUMBER: CATALYTIC NUCLEIC ACID AND ITS MEDICAL USE  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: PCT/IL97/00282  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: IL119135  
PRIOR FILING DATE: 1996-08-26  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: Patent In Ver. 2.1  
LENGTH: 30  
TYPE: RNA  
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US-09-257-503A-30  
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Matches 33; Conservative 9; Mismatches 8; Indels 0; Gaps 0;  
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US-09-257-503A-24  
Sequence 24, Application US/09257503A  
Patent No. 6387617  
GENERAL INFORMATION:  
APPLICANT: ASHER, Nathan  
APPLICANT: ELKHOCHINSKY, Yaron  
FILE REFERENCE: ASHER-2  
CURRENT APPLICATION NUMBER: CATALYTIC NUCLEIC ACID AND ITS MEDICAL USE  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: PCT/IL97/00282  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: IL119135  
PRIOR FILING DATE: 1996-08-26  
NUMBER OF SEQ ID NOS: 39  
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US-09-257-503A-27  
Sequence 27, Application US/09257503A  
Patent No. 6387617  
GENERAL INFORMATION:  
APPLICANT: ASHER, Nathan  
APPLICANT: ELKHOCHINSKY, Yaron  
FILE REFERENCE: ASHER-2  
CURRENT APPLICATION NUMBER: CATALYTIC NUCLEIC ACID AND ITS MEDICAL USE  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: PCT/IL97/00282  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: IL119135  
PRIOR FILING DATE: 1996-08-26  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: Patent In Ver. 2.1  
LENGTH: 27  
TYPE: RNA  
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Best Local Similarity 28.4%; Score 37.2; DB 4; Length 125;  
Matches 33; Conservative 9; Mismatches 8; Indels 0; Gaps 0;  
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Db 4 AATCTATCTAAACGGGGAACCTCTCTAGTAGACAAATCCCGTCTAAATTA 78  
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US-09-257-503A-28  
Sequence 28, Application US/09257503A  
Patent No. 6387617  
GENERAL INFORMATION:  
APPLICANT: ASHER, Nathan  
APPLICANT: ELKHOCHINSKY, Yaron  
FILE REFERENCE: ASHER-2  
CURRENT APPLICATION NUMBER: CATALYTIC NUCLEIC ACID AND ITS MEDICAL USE  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: PCT/IL97/00282  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: IL119135  
PRIOR FILING DATE: 1996-08-26  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: Patent In Ver. 2.1  
LENGTH: 28  
TYPE: RNA  
ORGANISM: Humanus  
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```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 800 Kb storage

COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,957
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/134,028
FILING DATE: 10 OCTOBER 1993
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA: 07/536,428
APPLICATION NUMBER: 11-JUNE-1990
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SBO ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-443-957-37

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RESULT 8
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; Sequence 6, Application US/08443957
; Patent No. 5580737
; GENERAL INFORMATION:
; APPLICANT: Barry Polisky
; APPLICANT: Robert Jenison
; APPLICANT: Larry Gold
; TITLE OF INVENTION: HIGH-AFFINITY NUCLEIC ACID LIGANDS THAT
; TITLE OF INVENTION: DISCRIMINATE BETWEEN THEOPHYLLINE AND
; TITLE OF INVENTION: CAFFEINE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 800 Kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:

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RESULT 9  
 US-08-825-852-20/c  
 Sequence 20, Application US/08825852  
 Patent No. 6121416  
 GENERAL INFORMATION:  
 APPLICANT: Clark, Ross G1  
 APPLICANT: Lowman, Henry B.  
 APPLICANT: Robinson, Iain C.A.F.  
 TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
 NUMBER OF SEQUENCES: 79  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Winpatin (genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/825,852  
 FILING DATE: 04-Apr-1997  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hasak, Janet E.  
 REGISTRATION NUMBER: 28,616  
 REFERENCE/DOCKET NUMBER: P1071  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-9861  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5140 base pairs  
 TYPE: Nucleic Acid  
 STRANDEDNESS: Single

Query Match	21.7%;	Score 28.4;	DB 3;	Length 5140;
Best Local Similarity	53.6%;	Pred. No. 0.55;		
Matches 59;	Conservative	0;	Mismatches 51.	Indels 0

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	68	GGTCAATATTTACACAGATCGCTTATGCTTGGCAGATAAATGCTT	117
QY			
Db	2376	GGCGAAGGCTCATCAGCGTGCTGCTTAACGAGTATCAAGATGTGCTT	2327

sequence 20, Application US/09052888  
; Patent No. 6251865

GENERAL INFORMATION:  
APPLICANT: Clark, Ross G.I  
APPLICANT: Lowman, Henry B.  
APPLICANT: Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-Like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94020

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1 COMPUTER READABLE FORM:
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3 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
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5 COMPUTER: IBM PC compatible
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7 OPERATING SYSTEM: PC-DOS/MS-DOS
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9 SOFTWARE: winpatln (Genentech)
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11 CURRENT APPLICATION DATA:
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13 APPLICATION NUMBER: US/09/052,888
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15 FILING DATE: 31-Mar-1998
16
17 CLASSIFICATION: 51A
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19 ATTORNEY/AGENT INFORMATION:
20
21 NAME: Hasak, Janet E.
22
23 REGISTRATION NUMBER: 28,616
24
25 REFERENCE/DOCKET NUMBER: P1071P1
26
27 TELECOMMUNICATION INFORMATION:
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29 TELEPHONE: 650/225-1896
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31 TELEFAX: 650/952-9881
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33 INFORMATION FOR SEQ ID NO: 20:
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35 SEQUENCE CHARACTERISTICS:
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37 LENGTH: 5140 base pairs
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39 TYPE: Nucleic Acid
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41 STRANDEDNESS: Single
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43 TOPOLOGY: Linear
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Query Match	Score	DB	Length
Best Local Similarity	21.7%	4	5140;
	53.68;		
	Pred. No. 0	55.	

	Indels	Gaps
QY 8 TATAAGTGACTTATACCTGTATATCTATCTAACGGGAACTCTGTAGTAGACATCC	67	
Db 2436 TTTAACAAAATTTTACCGCGAATTTTACAAAATATTAACGTTTAAATTTCCGATCCT	2377	
QY 68 GTGCTAATTTATACCAGCATGCTTGATGCCCTTGACATTAATGCCCT	117	
Db 2376 GCGGTAAGCTCATCAGCGTGTGCTGTAAACGATTACAGATCTCTGCCCT	2327	

RESULT 11  
US-08-887-352B-1/c  
; Sequence 1, Application US/08887352B

Patent No. 5994511  
GENERAL INFORMATION:  
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
TITLE OF INVENTION: Improving Polypeptides  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,352B  
FILING DATE: 03-Jul-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Syboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P1123  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6127 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Double  
TOPOLOGY: Circular  
US-08-887-352B-1

Query Match 21.7%; Score 28.4; DB 2; Length 6127;  
Best Local Similarity 53.6%; Pred. No. 0.59;  
Matches 59; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 8 TATAAGTGACTTATACCTGTAATCTATCTAAGCGGAGACCTCTCTAGTACATCC 67  
DB 3423 TTTAACAAAATTTTAAACGGGAATTTTAAACAAATTTTAAACGTTTCCGATCCT 3364  
QY 68 GTGCTAATTTATACAGCATCGTCTTGATGCCCTTGCGAGATAATGCT 117  
DB 3363 GCGGTAAAGCTATCAGCGTGTCTGTGAAGCGATTTCAGATGTCTGCT 3314

RESULT 12  
US-09-109-207C-1/C  
Sequence 1, Application US/09109207C  
Patent No. 6172213  
GENERAL INFORMATION:  
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
FILE REFERENCE: P1123R1  
CURRENT APPLICATION NUMBER: US/09/109,207C  
CURRENT FILING DATE: 1998-06-30  
PRIOR APPLICATION NUMBER: US 60/051,554  
PRIOR FILING DATE: 1997-07-03  
NUMBER OF SEQ ID NOS: 44  
SEQ ID NO 1  
LENGTH: 6127  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
NAME/KEY: Artificial  
LOCATION: 1-6127  
OTHER INFORMATION: Expression plasmid  
US-09-109-207C-1

Query Match 21.7%; Score 28.4; DB 4; Length 6127;  
Best Local Similarity 53.6%; Pred. No. 0.59;  
Matches 59; Conservative 0; Mismatches 51; Indels 0; Gaps 0;  
QY 8 TATAAGTGACTTATACCTGTAATCTATCTAAGCGGAGACCTCTCTAGTACATCC 67  
DB 3423 TTTAACAAAATTTTAAACGGGAATTTTAAACAAATTTTAAACGTTTCCGATCCT 3364  
QY 68 GTGCTAATTTATACAGCATCGTCTTGATGCCCTTGCGAGATAATGCT 117  
DB 3363 GCGGTAAAGCTATCAGCGTGTCTGTGAAGCGATTTCAGATGTCTGCT 3314  
RESULT 13  
US-09-296-005-1/C  
Sequence 1, Application US/09296005  
Patent No. 6290957  
GENERAL INFORMATION:  
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
FILE REFERENCE: P1123C1r  
CURRENT APPLICATION NUMBER: US/09/296,005  
CURRENT FILING DATE: 1999-04-21  
EARLIER APPLICATION NUMBER: US 08/887,352  
EARLIER FILING DATE: 1997-07-02  
NUMBER OF SEQ ID NOS: 26  
SEQ ID NO 1  
LENGTH: 6127  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
NAME/KEY: Artificial Sequence  
LOCATION: 1-6127  
OTHER INFORMATION: Expression plasmid  
US-09-296-005-1

Query Match 21.7%; Score 28.4; DB 4; Length 6127;  
Best Local Similarity 53.6%; Pred. No. 0.59;  
Matches 59; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 8 TATAAGTGACTTATACCTGTAATCTATCTAAGCGGAGACCTCTCTAGTACATCC 67  
DB 3423 TTTAACAAAATTTTAAACGGGAATTTTAAACAAATTTTAAACGTTTCCGATCCT 3364  
QY 68 GTGCTAATTTATACAGCATCGTCTTGATGCCCTTGCGAGATAATGCT 117  
DB 3363 GCGGTAAAGCTATCAGCGTGTCTGTGAAGCGATTTCAGATGTCTGCT 3314

RESULT 14  
US-08-468-819-89/C  
Sequence 89, Application US/08468819  
Patent No. 5671723  
GENERAL INFORMATION:  
APPLICANT: Strieter, Robert M.  
APPLICANT: Polyneri, Peter J.  
APPLICANT: Kunkel, Steven L.  
TITLE OF INVENTION: CXG Chemokines as Regulators of  
TITLE OF INVENTION: Angiogenesis  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: US  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

Query Match	20.9%	Score 27.4; DB 2;	Length 297;
Best Local Similarity	69.8%	Pred. No. 0.41;	
Matches	37;	Conservative	0; Mismatches 16; Indels 0; Gaps 0;
OY	52	TCTTGTGACACATCCCGTCTTAATTAACACAGATCGTCGTGAGCCCTTG	104
Db	288	TCTTTTGGACATTCCTCTGCTACACGCTTGAATTAATTCGTGAGCCCTTCG	236

RESULT 15  
 US-08-493-638-5/c  
 Sequence 5, Application US/08493638  
 Patent No. 5824299  
 GENERAL INFORMATION:  
 APPLICANT: Luster, Andrew  
 APPLICANT: Leder, Philip  
 TITLE OF INVENTION: MODULATION OF ENDOTHELIAL CELL  
 TITLE OF INVENTION: PROLIFERATION  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/493,638  
 FILING DATE: 22-JUN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Clark, Paul T.  
 REGISTRATION NUMBER: 30,162  
 REFERENCE/DOCKET NUMBER: 00383/027001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1185 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: CDS

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:      LOCATION:      80...374
US-08-493-638-5

Query Match          20.9%; Score 27.4; DB 1; Length 1185;
Best Local Similarity 69.8%; Pred. No. 0.72;
Matches 37; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY      52  TCTAGTAGACAAATCCCGTGTCTAAATATTATACAGACATCGCTTTGATGCCCTTGG 104
      |||  |||||  |||  |||||  |||  |||  |||  |||||  |||||  |||  |
Db      367  TCTTTTAGACATTTCTCCTTGTAACTGCGCTTTGAGTAATTCCTTGAGGCGCTTCG 315

Search completed: July 13, 2003, 22:16:09
Job time : 38 secs

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Search completed: July 13, 2003, 22:16:09  
Job time : 38 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 13, 2003, 22:13:22 ; Search time 103 Seconds  
(without alignments)  
2008.237 Million cell updates/sec

Title: US-09-661-658b-2

Perfect score: 131  
Sequence: 1 gcttgagtaagtgactt.....atgcctaacgactacccctt 131

Scoring table: IDENTITY\_NUC  
Gap 10.0 , Gapext 1.0

Searched: 1105431 seqs, 789497651 residues

Total number of hits satisfying chosen parameters: 2210862

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
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13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	131	100.0	131	US-09-883-119A-2	Sequence 2, Appl
2	131	100.0	131	US-09-883-119A-20	Sequence 20, Appl
3	127.4	97.3	131	US-09-883-119A-5	Sequence 5, Appl
4	109	83.2	133	US-09-883-119A-21	Sequence 21, Appl
5	107	81.7	129	US-09-883-119A-23	Sequence 23, Appl
6	87	66.4	119	US-09-883-119A-22	Sequence 22, Appl
7	86.4	66.0	117	US-09-883-119A-25	Sequence 25, Appl
8	83.4	63.7	115	US-09-883-119A-24	Sequence 24, Appl
9	82.2	62.7	122	US-09-883-119A-30	Sequence 30, Appl
10	81.4	62.1	107	US-09-883-119A-28	Sequence 28, Appl
11	80.6	61.5	122	US-09-883-119A-16	Sequence 16, Appl
12	79.8	60.9	107	US-09-883-119A-29	Sequence 29, Appl
13	78.2	59.7	124	US-09-883-119A-31	Sequence 31, Appl
14	76	58.0	94	US-09-883-119A-19	Sequence 19, Appl
15	49.6	37.9	144	US-09-883-119A-26	Sequence 26, Appl
16	45.8	35.0	140	US-09-883-119A-27	Sequence 27, Appl
17	37.2	28.4	59	US-09-326-956-2	Sequence 47, Appl
18	31.4	24.0	108	US-09-952-680A-47	Sequence 47, Appl
19	31.4	24.0	120	US-09-952-680A-46	Sequence 46, Appl

20	31.2	23.8	44	9	US-09-872-696A-62	Sequence 62, Appl
21	31.2	23.8	44	10	US-09-231-235-62	Sequence 62, Appl
22	31.2	23.8	44	10	US-09-797-518A-62	Sequence 62, Appl
23	30.8	23.5	38	9	US-09-872-696A-61	Sequence 61, Appl
24	30.8	23.5	38	10	US-09-231-235-61	Sequence 61, Appl
25	30.8	23.5	38	10	US-09-797-518A-61	Sequence 61, Appl
26	29.2	22.3	921	9	US-10-106-698-174	Sequence 174, Appl
27	29	22.1	1503841	9	US-09-946-807-1	Sequence 1, Appl
28	29	22.1	1503841	10	US-09-795-668-1	Sequence 1, Appl
29	29	22.1	1503841	10	US-09-795-668-1	Sequence 1, Appl
30	28.4	21.7	5140	9	US-09-858-938B-1	Sequence 99, Appl
31	28.4	21.7	6072	10	US-09-056-160B-99	Sequence 1, Appl
32	28.4	21.7	6127	10	US-09-920-171-1	Sequence 36, Appl
33	28.2	21.5	84539	10	US-09-962-436-36	Sequence 89, Appl
34	27.4	20.9	1172	9	US-10-104-755-89	Sequence 165, Appl
35	27.4	20.9	1172	9	US-09-954-531-165	Sequence 412, Appl
36	27.4	20.9	1172	9	US-09-954-531-374	Sequence 250, Appl
37	27.4	20.9	1172	10	US-10-177-293-412	Sequence 282, Appl
38	27.4	20.9	1172	10	US-09-833-790-250	Sequence 2610, Appl
39	27.4	20.9	1172	10	US-09-962-436-282	Sequence 2, Appl
40	27.4	20.9	1452	10	US-09-738-626-2610	Sequence 2687, Appl
41	27.4	20.9	2653	9	US-09-892-867-2	Sequence 7468, Appl
42	27.4	20.9	3309400	9	US-09-738-626-1	Sequence 1075, Appl
43	27	20.6	1623	9	US-09-938-842A-2687	
44	26.2	20.0	477	9	US-10-198-846-7468	
45	26.2	20.0	1635	9	US-10-092-154-1075	

## ALIGNMENTS

RESULT 1  
US-09-883-119A-2  
Sequence 2, Application US/09883119A  
Publication No. US20030104520A1  
GENERAL INFORMATION:  
APPLICANT: The University of Texas System Board of Regents  
TITLE OF INVENTION: Regulator, Catalytically Active Nucleic Acids  
FILE REFERENCE: 119927-1050  
CURRENT APPLICATION NUMBER: US/09/883, 119A  
CURRENT FILING DATE: 2000-06-14  
PRIOR APPLICATION NUMBER: 60/212,097  
PRIOR FILING DATE: 2000-06-15  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 131  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Engineered Aptazyme  
US-09-883-119A-2

Query Match 100.0%; Score 131; DB 9; Length 131;  
Best Local Similarity 100.0%; Pred No. 1.8e-37;  
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GCCTGAGTAAAGTGACTTAACTGTAATCTAAACGGGAACTCTAGTAGA	60
DB	1	GCCTGAGTAAAGTGACTTAACTGTAATCTAAACGGGAACTCTAGTAGA	60
QY	61	CAATCCGCTGCTAAATATACACGATGCTGATGCTGCGAGATTAATGCTTAAC	120
DB	61	CAATCCGCTGCTAAATATATACACGATGCTGATGCTGCGAGATTAATGCTTAAC	120
QY	121	GACTATCCCTT 131	
DB	121	GACTATCCCTT 131	

RESULT 2  
US-09-883-119A-20  
Sequence 20, Application US/09883119A

Publication No. US20030104520A1  
GENERAL INFORMATION:  
APPLICANT: The University of Texas System Board of Regents  
TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids  
FILE REFERENCE: 119927-1050  
CURRENT APPLICATION NUMBER: US/09/883,119A  
PRIORITY FILING DATE: 2000-06-14  
PRIORITY FILING DATE: 2000-06-15  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 20  
LENGTH: 131  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: oligonucleotide  
US-09-883-119A-20

Query Match  
Best Local Similarity 100.0%; Score 131; DB 9; Length 131;  
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGAGTATAGTACTTATCTATCTAATCTAATACGGGGAACCTCTCTAGTAGA 60  
DB 1 GCCTGAGTATAGTACTTATCTAATCTAATACGGGGAACCTCTCTAGTAGA 60  
QY 61 CAATCCCGTCTAATTAATTAACAGCATGCTTGTGATGCCCTTGAGATAATGCCCTAAC 120  
DB 61 CAATCCCGTCTAATTAATTAACAGCATGCTTGTGATGCCCTTGAGATAATGCCCTAAC 120  
QY 121 GACTATCCCTT 131  
DB 121 GACTATCCCTT 131

## RESULT 3

US-09-883-119A-5  
Sequence 5, Application US/09883119A  
Publication No. US20030104520A1  
GENERAL INFORMATION:  
APPLICANT: The University of Texas System Board of Regents  
TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids  
FILE REFERENCE: 119927-1050  
CURRENT APPLICATION NUMBER: US/09/883,119A  
PRIORITY FILING DATE: 2000-06-14  
PRIORITY FILING DATE: 2000-06-15  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 131  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Engineered Aptazyme  
NAME/KEY: misc.feature  
LOCATION: (77)-(77)  
OTHER INFORMATION: n-a,c,t, or g  
NAME/KEY: misc.feature  
LOCATION: (108)-(108)  
OTHER INFORMATION: n-a,c,t, or g  
US-09-883-119A-5

Query Match  
Best Local Similarity 97.3%; Score 127.4; DB 9; Length 131;  
Matches 128; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCTGAGTATAGTACTTATCTAATCTAATACGGGGAACCTCTCTAGTAGA 60  
DB 1 GCCTGAGTATAGTACTTATCTAATCTAATACGGGGAACCTCTCTAGTAGA 60

QY 61 CAATCCCGTCTAATTAATTAACAGCATGCTTGTGATGCCCTTGAGATAATGCCCTAAC 120  
DB 61 CAATCCCGTCTAATTAATTAACAGCATGCTTGTGATGCCCTTGAGATAATGCCCTAAC 120  
QY 121 GACTATCCCTT 131  
DB 121 GACTATCCCTT 131

## RESULT 4

US-09-883-119A-21  
Sequence 21, Application US/09883119A  
Publication No. US20030104520A1  
GENERAL INFORMATION:  
APPLICANT: The University of Texas System Board of Regents  
TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids  
FILE REFERENCE: 119927-1050  
CURRENT APPLICATION NUMBER: US/09/883,119A  
PRIORITY FILING DATE: 2000-06-14  
PRIORITY FILING DATE: 2000-06-15  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 21  
LENGTH: 133  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: oligonucleotide  
US-09-883-119A-21

Query Match  
Best Local Similarity 83.2%; Score 109; DB 9; Length 133;  
Matches 131; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 GCCTGAGTATAGTACTTATCTAATCTAATACGGGGAACCTCTCTAGTAGA 60  
DB 1 GCCTGAGTATAGTACTTATCTAATCTAATACGGGGAACCTCTCTAGTAGA 60  
QY 61 CAATCCCGTCTAATTAATTAACAGCATGCTTGTGATGCCCTTGAGATAATGCCCTAAC 118  
DB 61 CAATCCCGTCTAATTAATTAACAGCATGCTTGTGATGCCCTTGAGATAATGCCCTAAC 120  
QY 119 AGGACTATCCCTT 131  
DB 121 AGGACTATCCCTT 133

## RESULT 5

US-09-883-119A-23  
Sequence 23, Application US/09883119A  
Publication No. US20030104520A1  
GENERAL INFORMATION:  
APPLICANT: The University of Texas System Board of Regents  
TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids  
FILE REFERENCE: 119927-1050  
CURRENT APPLICATION NUMBER: US/09/883,119A  
PRIORITY FILING DATE: 2000-06-14  
PRIORITY FILING DATE: 2000-06-15  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 23  
LENGTH: 129  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: oligonucleotide  
US-09-883-119A-23

Query Match  
Best Local Similarity 81.7%; Score 107; DB 9; Length 129;  
Matches 128; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



Matches 129: Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 GCCTGAGTATAGTGAAGTCTTACTTGAATCTATCTAAACGGGGAACCTCTCTAGTAGA 60  
 1 GCCTGAGTATAGTGAAGTCTTACTTGAATCTATCTAAACGGGGAACCTCTCTAGTAGA 60  
 Db 61 CAATCCCGTGTCTAAATTTATACAGCATGCTTGTATGCCCTTGGCAGATTAATGCTTAAC 120  
 61 CAATCCCGTGTCTAAATTTATACAGCATGCTTGTATGCCCTTGGCAGATTAATGCTTAAC 118  
 QY 121 GACTATCCCTT 131  
 119 GACTATCCCTT 129

RESULT 6  
 US-09-883-119A-22  
 ; Sequence 22, Application US/09883119A  
 ; Publication No. US20030104520A1

GENERAL INFORMATION:

APPLICANT: The University of Texas System Board of Regents  
 TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids

FILE REFERENCE: 119927-1050  
 CURRENT APPLICATION NUMBER: US/09/883,119A

PRIOR FILING DATE: 2000-06-14  
 PRIOR APPLICATION NUMBER: 60/212,097

NUMBER OF SEQ ID NOS: 44  
 SOFTWARE: PatentIn version 3.1

SEQ ID NO 22  
 LENGTH: 119

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:  
 OTHER INFORMATION: oligonucleotide

US-09-883-119A-22

Query Match 66.4%; Score 87; DB 9; Length 119;  
 Best Local Similarity 90.8%; Pred. No. 1.3e-21;  
 Matches 119: Conservative 0; Mismatches 0; Indels 12; Gaps 2;

QY 1 GCCTGAGTATAGTGAAGTCTTACTTGAATCTATCTAAACGGGGAACCTCTCTAGTAGA 60  
 1 GCCTGAGTATAGTGAAGTCTTACTTGAATCTATCTAAACGGGGAACCTCTCTAGTAGA 60  
 Db 61 CAATCCCGTGTCTAAATTTATACAGCATGCTTGTATGCCCTTGGCAGATTAATGCTTAAC 120  
 61 CAATCCCGTGTCTAAATTTATACAGCATGCTTGTATGCCCTTGGCAGATTAATGCTTAAC 108  
 QY 121 GACTATCCCTT 131  
 109 GACTATCCCTT 119

RESULT 7  
 US-09-883-119A-25  
 ; Sequence 25, Application US/09883119A  
 ; Publication No. US20030104520A1

GENERAL INFORMATION:

APPLICANT: The University of Texas System Board of Regents  
 TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids

FILE REFERENCE: 119927-1050  
 CURRENT APPLICATION NUMBER: US/09/883,119A

PRIOR FILING DATE: 2000-06-14  
 PRIOR APPLICATION NUMBER: 60/212,097

NUMBER OF SEQ ID NOS: 44  
 SOFTWARE: PatentIn version 3.1

SEQ ID NO 25  
 LENGTH: 117

TYPE: DNA

ORGANISM: Artificial Sequence  
 FEATURE:

OTHER INFORMATION: oligonucleotide  
 US-09-883-119A-25

Query Match 66.0%; Score 86.4; DB 9; Length 117;  
 Best Local Similarity 89.2%; Pred. No. 2e-21;  
 Matches 107: Conservative 0; Mismatches 6; Indels 7; Gaps 1;

QY 1 GCCTGAGTATAGTGAAGTCTTACTTGAATCTATCTAAACGGGGAACCTCTCTAGTAGA 60  
 1 GCCTGAGTATAGTGAAGTCTTACTTGAATCTATCTAAACGGGGAACCTCTCTAGTAGA 60  
 Db 61 CAATCCCGTGTCTAAATTTATACAGCATGCTTGTATGCCCTTGGCAGATTAATGCTTAAC 120  
 61 CAATCCCGTGTCTAAATTTATACAGCATGCTTGTATGCCCTTGGCAGATTAATGCTTAAC 113

RESULT 8  
 US-09-883-119A-24  
 ; Sequence 24, Application US/09883119A  
 ; Publication No. US20030104520A1

GENERAL INFORMATION:

APPLICANT: The University of Texas System Board of Regents  
 TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids

FILE REFERENCE: 119927-1050  
 CURRENT APPLICATION NUMBER: US/09/883,119A

PRIOR FILING DATE: 2000-06-14  
 PRIOR APPLICATION NUMBER: 60/212,097

NUMBER OF SEQ ID NOS: 44  
 SOFTWARE: PatentIn version 3.1

SEQ ID NO 24  
 LENGTH: 115

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:  
 OTHER INFORMATION: oligonucleotide

US-09-883-119A-24

Query Match 63.7%; Score 83.4; DB 9; Length 115;  
 Best Local Similarity 91.9%; Pred. No. 2.5e-20;  
 Matches 102: Conservative 0; Mismatches 1; Indels 8; Gaps 1;

QY 1 GCCTGAGTATAGTGAAGTCTTACTTGAATCTATCTAAACGGGGAACCTCTCTAGTAGA 60  
 1 GCCTGAGTATAGTGAAGTCTTACTTGAATCTATCTAAACGGGGAACCTCTCTAGTAGA 60  
 Db 61 CAATCCCGTGTCTAAATTTATACAGCATGCTTGTATGCCCTTGGCAGATTAATGCTTAAC 111  
 61 CAATCCCGTGTCTAAATTTATACAGCATGCTTGTATGCCCTTGGCAGATTAATGCTTAAC 103

RESULT 9  
 US-09-883-119A-30  
 ; Sequence 30, Application US/09883119A  
 ; Publication No. US20030104520A1

GENERAL INFORMATION:

APPLICANT: The University of Texas System Board of Regents  
 TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids

FILE REFERENCE: 119927-1050  
 CURRENT APPLICATION NUMBER: US/09/883,119A

PRIOR FILING DATE: 2000-06-14  
 PRIOR APPLICATION NUMBER: 60/212,097

NUMBER OF SEQ ID NOS: 44  
 SOFTWARE: PatentIn version 3.1

SEQ ID NO 30  
 LENGTH: 122

TYPE: DNA

ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: oligonucleotide

US-09-883-119A-30

Query Match 62.7%; Score 82.2; DB 9; Length 122;  
Best Local Similarity 83.2%; Pred. No. 6,8e-20;  
Matches 109; Conservative 0; Mismatches 13; Indels 9; Gaps 1;

QY 1 GCCTAGATTAAGGAGCTTATCTATCTATCTAATCAAGGGGAACTCTCTAGTAGA 60  
DB 1 GCCTAGATTAAGGAGCTTATCTATCTAATCAAGGGGAACTCTCTAGTAGA 60  
QY 61 CAATCCCGTCTAATTAATTAACCAATCGCTTGTATGACCTTGGCAGATTAATGCTTAAC 120  
DB 61 CAATCCCGTCTAATTAATTAACCAATCGCTTGTATGACCTTGGCAGATTAATGCTTAAC 111  
QY 121 GACTATCCCTT 131  
DB 112 GACTATCCCTT 122

## RESULT 10

US-09-883-119A-28  
Sequence 28, Application US/09883119A  
Publication No. US20030104520A1  
GENERAL INFORMATION:  
APPLICANT: The University of Texas System Board of Regents  
TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids  
FILE REFERENCE: 119927-1050  
CURRENT APPLICATION NUMBER: US/09/883,119A  
PRIOR FILING DATE: 2000-06-14  
PRIOR APPLICATION NUMBER: 60/212,097  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 28  
LENGTH: 107  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: oligonucleotide  
US-09-883-119A-28

Query Match 62.1%; Score 81.4; DB 9; Length 107;  
Best Local Similarity 97.2%; Pred. No. 1.3e-19;  
Matches 104; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 27 GTAATCTATCTAAGGGGAACTCTCTAGTAGACAATCCCGTCTAATT-ATACCAGC 85  
DB 1 GTAATCTATCTAAGGGGAACTCTCTAGTAGACAATCCCGTCTAATTGATACCAGC 60  
QY 86 ATCGTCTGATGCCCTTGGCAG-ATAAATGCCCTAAGCACTATCCCTT 131  
DB 61 ATCGTCTGATGCCCTTGGCAGCAATTAATGCCCTAAGCACTATCCCTT 107

## RESULT 11

US-09-883-119A-16  
Sequence 16, Application US/09883119A  
Publication No. US20030104520A1  
GENERAL INFORMATION:  
APPLICANT: The University of Texas System Board of Regents  
TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids  
FILE REFERENCE: 119927-1050  
CURRENT APPLICATION NUMBER: US/09/883,119A  
PRIOR FILING DATE: 2000-06-14  
PRIOR APPLICATION NUMBER: 60/212,097  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 16  
LENGTH: 122  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Parental p6 construct  
US-09-883-119A-16

Query Match 61.5%; Score 80.6; DB 9; Length 122;  
Best Local Similarity 82.4%; Pred. No. 2.6e-19;  
Matches 108; Conservative 0; Mismatches 14; Indels 9; Gaps 1;

QY 1 GCCTAGATTAAGGAGCTTATCTATCTATCTAATCAAGGGGAACTCTCTAGTAGA 60  
DB 1 GCCTAGATTAAGGAGCTTATCTATCTAATCAAGGGGAACTCTCTAGTAGA 60  
QY 61 CAATCCCGTCTAATTAATTAACCAATCGCTTGTATGACCTTGGCAGATTAATGCTTAAC 120  
DB 61 CAATCCCGTCTAATTAATTAACCAATCGCTTGTATGACCTTGGCAGATTAATGCTTAAC 111  
QY 121 GACTATCCCTT 131  
DB 112 GACTATCCCTT 122

## RESULT 12

US-09-883-119A-29  
Sequence 29, Application US/09883119A  
Publication No. US20030104520A1  
GENERAL INFORMATION:  
APPLICANT: The University of Texas System Board of Regents  
TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids  
FILE REFERENCE: 119927-1050  
CURRENT APPLICATION NUMBER: US/09/883,119A  
PRIOR FILING DATE: 2000-06-14  
PRIOR APPLICATION NUMBER: 60/212,097  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 29  
LENGTH: 107  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: oligonucleotide  
US-09-883-119A-29

Query Match 60.9%; Score 79.8; DB 9; Length 107;  
Best Local Similarity 96.3%; Pred. No. 4.7e-19;  
Matches 103; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 27 GTAATCTATCTAAGGGGAACTCTCTAGTAGACAATCCCGTCTAATT-ATACCAGC 85  
DB 1 GTAATCTATCTAAGGGGAACTCTCTAGTAGACAATCCCGTCTAATTGATACCAGC 60  
QY 86 ATCGTCTGATGCCCTTGGCAG-ATAAATGCCCTAAGCACTATCCCTT 131  
DB 61 ATCGTCTGATGCCCTTGGTTCATTAATGCTTAAGCACTATCCCTT 107

## RESULT 13

US-09-883-119A-31  
Sequence 31, Application US/09883119A  
Publication No. US20030104520A1  
GENERAL INFORMATION:  
APPLICANT: The University of Texas System Board of Regents  
TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids  
FILE REFERENCE: 119927-1050  
CURRENT APPLICATION NUMBER: US/09/883,119A  
PRIOR FILING DATE: 2000-06-14  
PRIOR APPLICATION NUMBER: 60/212,097  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 31  
LENGTH: 124  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: oligonucleotide

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